

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 24, 2006, 10:29:45 ; Search time 18 Seconds
(without alignments)
7.444 Million cell updates/sec

Title: US-10-019-513-1

Perfect score: 49

Sequence: 1 STAPPVHV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 34777

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA_New.*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	9	6 US-10-401-386B-52	Sequence 52, Appl
2	49	100.0	9	6 US-10-517-784-35	Sequence 35, Appl
3	39	79.6	9	6 US-10-401-386B-56	Sequence 56, Appl
4	24	49.0	8	7 US-11-045-024-6286	Sequence 6286, Ap
5	24	49.0	8	7 US-11-045-024-6385	Sequence 6385, Ap
6	24	49.0	8	7 US-11-045-024-6286	Sequence 6286, Ap
7	24	49.0	8	7 US-11-045-024-9105	Sequence 9105, Ap
8	24	49.0	9	7 US-11-011-666-5	Sequence 5, Appl
9	24	49.0	9	7 US-11-045-024-146	Sequence 146, Appl
10	24	49.0	9	7 US-11-045-024-148	Sequence 148, Appl
11	24	49.0	9	7 US-11-045-024-2988	Sequence 2988, Ap
12	24	49.0	9	7 US-11-045-024-4112	Sequence 4112, Ap
13	24	49.0	9	7 US-11-045-024-4114	Sequence 4114, Ap
14	24	49.0	9	7 US-11-045-024-5659	Sequence 5659, Ap
15	24	49.0	9	7 US-11-045-024-6287	Sequence 6287, Ap
16	24	49.0	9	7 US-11-045-024-6387	Sequence 6387, Ap
17	24	49.0	9	7 US-11-045-024-8861	Sequence 8861, Ap
18	24	49.0	9	7 US-11-045-024-8862	Sequence 8862, Ap
19	24	49.0	9	7 US-11-045-024-9107	Sequence 9107, Ap
20	24	49.0	9	7 US-11-045-024-11134	Sequence 11134, A
21	23	46.9	7	7 US-11-031-737A-40	Sequence 40, Appl
22	23	46.9	7	7 US-11-031-482-40	Sequence 40, Appl
23	23	46.9	8	7 US-11-045-024-5300	Sequence 5300, Ap
24	23	46.9	8	7 US-11-045-024-6267	Sequence 6267, Ap
25	23	46.9	8	7 US-11-045-024-6353	Sequence 6353, Ap

26	23	46.9	8	7 US-11-045-024-7822	Sequence 7822, Ap
27	23	46.9	8	7 US-11-045-024-8826	Sequence 8826, Ap
28	23	46.9	8	7 US-11-045-024-9004	Sequence 9004, Ap
29	23	46.9	9	6 US-10-510-101-57	Sequence 57, Appl
30	23	46.9	9	6 US-10-510-101-58	Sequence 58, Appl
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34	23	46.9	9	6 US-10-510-101-175	Sequence 175, App
35	23	46.9	9	7 US-11-045-024-147	Sequence 147, App
36	23	46.9	9	7 US-11-045-024-149	Sequence 149, App
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38	23	46.9	9	7 US-11-045-024-1885	Sequence 1885, Ap
39	23	46.9	9	7 US-11-045-024-2987	Sequence 2987, Ap
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65	22	44.9	8	7 US-11-045-024-3	Sequence 3, Appl
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68	22	44.9	8	7 US-11-045-024-6187	Sequence 6187, Ap
69	22	44.9	9	7 US-11-045-024-601	Sequence 601, App
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71	22	44.9	9	7 US-11-045-024-6844	Sequence 6844, Ap
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73	22	44.9	9	7 US-11-045-024-8730	Sequence 8730, Ap
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85	21	42.9	9	6 US-10-895-064-1420	Sequence 1420, Ap
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89	21	42.9	9	7 US-11-045-024-7004	Sequence 7004, Ap
90	21	42.9	9	7 US-11-129-741-1420	Sequence 1420, Ap
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92	20	40.8	7	5 US-09-810-501-62	Sequence 62, Appl
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96	20	40.8	7	6 US-10-964-313-51	Sequence 51, Appl
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103	20	40.8	9	7	US-11-073-347-44	Sequence 44, Appl	176	18	36.7	7	6	US-10-485-788A-79	Sequence 79, Appl
104	20	40.8	9	7	US-11-045-024-1837	Sequence 1837, Ap	177	18	36.7	7	6	US-10-509-292-39	Sequence 39, Appl
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106	20	40.8	9	7	US-11-026-403-9	Sequence 9, Appli	179	18	36.7	7	7	US-11-051-453-15	Sequence 15, Appl
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109	19	38.8	6	7	US-11-121-613-393	Sequence 393, App	182	18	36.7	8	6	US-10-895-064-1553	Sequence 1553, Ap
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115	19	38.8	8	7	US-11-045-024-1075	Sequence 1075, Ap	188	18	36.7	8	7	US-11-045-024-2476	Sequence 2476, Ap
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122	19	38.8	8	7	US-11-045-024-11227	Sequence 11227, A	195	18	36.7	8	7	US-11-045-024-8713	Sequence 8713, Ap
123	19	38.8	8	7	US-11-045-024-11352	Sequence 11352, A	196	18	36.7	8	7	US-11-045-024-8745	Sequence 8745, Ap
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253	18	36.7	9	7	US-11-045-024-8692	Sequence 8692, Ap	326	17	34.7	9	6	US-10-925-366A-33	Sequence 33, Appl
254	18	36.7	9	7	US-11-045-024-9885	Sequence 9885, Ap	327	17	34.7	9	6	US-10-857-643-577	Sequence 577, App
255	18	36.7	9	7	US-11-045-024-11007	Sequence 11007, A	328	17	34.7	9	6	US-10-857-484-285	Sequence 285, App
256	18	36.7	9	7	US-11-045-024-11014	Sequence 11014, A	329	17	34.7	9	6	US-10-857-484-287	Sequence 287, App
257	18	36.7	9	7	US-11-045-024-11848	Sequence 11848, A	330	17	34.7	9	6	US-10-857-484-297	Sequence 297, App
258	18	36.7	9	7	US-11-045-024-13546	Sequence 13546, A	331	17	34.7	9	6	US-10-857-484-304	Sequence 304, App
259	18	36.7	9	7	US-11-045-024-13549	Sequence 13549, A	332	17	34.7	9	6	US-10-857-484-312	Sequence 312, App
260	18	36.7	9	7	US-11-045-024-13601	Sequence 13601, A	333	17	34.7	9	6	US-10-857-484-360	Sequence 360, App
261	18	36.7	9	7	US-11-045-024-13617	Sequence 13617, A	334	17	34.7	9	6	US-10-857-484-435	Sequence 435, App
262	18	36.7	9	7	US-11-045-024-13859	Sequence 13859, A	335	17	34.7	9	6	US-10-857-484-438	Sequence 438, App
263	18	36.7	9	7	US-11-045-024-13861	Sequence 13861, A	336	17	34.7	9	6	US-10-857-484-443	Sequence 443, App
264	18	36.7	9	7	US-11-045-024-13959	Sequence 13959, A	337	17	34.7	9	6	US-10-857-484-444	Sequence 444, App
265	18	36.7	9	7	US-11-045-024-14030	Sequence 14030, A	338	17	34.7	9	6	US-10-857-484-450	Sequence 450, App
266	18	36.7	9	7	US-11-045-024-14327	Sequence 14327, A	339	17	34.7	9	6	US-10-857-484-451	Sequence 451, App
267	18	36.7	9	7	US-11-045-024-14453	Sequence 14453, A	340	17	34.7	9	6	US-10-857-484-452	Sequence 452, App
268	18	36.7	9	7	US-11-146-854-20	Sequence 20, Appl	341	17	34.7	9	6	US-10-857-484-455	Sequence 455, App
269	18	36.7	9	7	US-11-026-403-32	Sequence 32, Appl	342	17	34.7	9	6	US-10-857-484-876	Sequence 876, App
270	18	36.7	9	7	US-11-033-039-303	Sequence 303, App	343	17	34.7	9	6	US-10-857-484-876	Sequence 876, App
271	18	36.7	9	7	US-11-033-039-308	Sequence 308, App	344	17	34.7	9	6	US-10-857-484-918	Sequence 918, App
272	18	36.7	9	7	US-11-033-039-464	Sequence 464, App	345	17	34.7	9	6	US-10-857-484-923	Sequence 923, App
273	18	36.7	9	7	US-11-033-039-657	Sequence 657, App	346	17	34.7	9	6	US-10-857-484-1005	Sequence 1005, Ap
274	18	36.7	9	7	US-11-018-868-78	Sequence 78, Appl	347	17	34.7	9	6	US-10-857-484-1010	Sequence 1010, Ap
275	18	36.7	9	7	US-11-018-868-84	Sequence 84, Appl	348	17	34.7	9	6	US-10-857-484-1013	Sequence 1013, Ap
276	18	36.7	9	7	US-11-247-423-31	Sequence 31, Appl	349	17	34.7	9	6	US-10-857-484-1018	Sequence 1018, Ap
277	18	36.7	9	7	US-11-247-423-70	Sequence 70, Appl	350	17	34.7	9	6	US-10-857-484-1020	Sequence 1020, Ap
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279	17	34.7	5	6	US-10-485-788A-77	Sequence 77, Appl	352	17	34.7	9	6	US-10-857-484-1026	Sequence 1026, Ap
280	17	34.7	5	6	US-10-895-064-2176	Sequence 2176, Ap	353	17	34.7	9	6	US-10-857-484-1027	Sequence 1027, Ap
281	17	34.7	5	6	US-11-121-612-391	Sequence 391, App	354	17	34.7	9	6	US-10-857-484-1428	Sequence 1428, Ap
282	17	34.7	5	6	US-11-129-741-2176	Sequence 2176, Ap	355	17	34.7	9	6	US-10-857-484-1448	Sequence 1448, Ap
283	17	34.7	6	6	US-10-986-501-321	Sequence 321, App	356	17	34.7	9	6	US-10-857-484-1477	Sequence 1477, Ap
284	17	34.7	6	7	US-11-032-773-724	Sequence 724, App	357	17	34.7	9	6	US-10-857-484-1498	Sequence 1498, Ap
285	17	34.7	6	7	US-11-121-612-404	Sequence 404, App	358	17	34.7	9	6	US-10-857-484-1506	Sequence 1506, Ap
286	17	34.7	6	7	US-11-078-256-4	Sequence 4, Appl	359	17	34.7	9	6	US-10-857-484-1575	Sequence 1575, Ap
287	17	34.7	6	7	US-10-467-657-9078	Sequence 9078, Ap	360	17	34.7	9	6	US-10-857-484-1579	Sequence 1579, Ap
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289	17	34.7	7	7	US-11-106-932-140	Sequence 140, App	362	17	34.7	9	6	US-10-857-484-1586	Sequence 1586, Ap
290	17	34.7	7	7	US-11-078-256-6	Sequence 6, Appl	363	17	34.7	9	6	US-10-857-484-1588	Sequence 1588, Ap
291	17	34.7	7	7	US-11-129-741-1514	Sequence 1514, Ap	364	17	34.7	9	6	US-10-857-484-1593	Sequence 1593, Ap
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295	17	34.7	8	7	US-11-045-024-3172	Sequence 3172, Ap	368	17	34.7	9	6	US-10-857-484-2004	Sequence 2004, Ap
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303	17	34.7	8	7	US-11-045-024-5414	Sequence 5414, Ap	376	17	34.7	9	6	US-10-857-484-2145	Sequence 2145, Ap
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305	17	34.7	8	7	US-11-045-024-6811	Sequence 6811, Ap	378	17	34.7	9	6	US-10-857-484-2151	Sequence 2151, Ap
306	17	34.7	8	7	US-11-045-024-7215	Sequence 7215, Ap	379	17	34.7	9	6	US-10-857-484-2152	Sequence 2152, Ap
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308	17	34.7	8	7	US-11-045-024-7300	Sequence 7300, Ap	381	17	34.7	9	6	US-10-857-484-2545	Sequence 2545, Ap
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393	17	34.7	9	6	US-10-857-484-3255	Sequence 3255, Ap	466	17	34.7	9	6	US-10-857-484-5161	Sequence 5161, Ap
394	17	34.7	9	6	US-10-857-484-3257	Sequence 3257, Ap	467	17	34.7	9	6	US-10-857-484-5162	Sequence 5162, Ap
395	17	34.7	9	6	US-10-857-484-3264	Sequence 3264, Ap	468	17	34.7	9	6	US-10-857-484-5165	Sequence 5165, Ap
396	17	34.7	9	6	US-10-857-484-3266	Sequence 3266, Ap	469	17	34.7	9	6	US-10-857-484-5168	Sequence 5168, Ap
397	17	34.7	9	6	US-10-857-484-3271	Sequence 3271, Ap	470	17	34.7	9	6	US-10-857-484-5169	Sequence 5169, Ap
398	17	34.7	9	6	US-10-857-484-3273	Sequence 3273, Ap	471	17	34.7	9	6	US-10-857-484-5219	Sequence 5219, Ap
399	17	34.7	9	6	US-10-857-484-3277	Sequence 3277, Ap	472	17	34.7	9	6	US-10-857-484-5219	Sequence 5219, Ap
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436	17	34.7	9	6	US-10-857-484-4522	Sequence 4522, Ap	509	17	34.7	9	7	US-11-045-024-10358	Sequence 10358, A
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439	17	34.7	9	6	US-10-857-484-4572	Sequence 4572, Ap	512	17	34.7	9	7	US-11-045-024-12145	Sequence 12145, A
440	17	34.7	9	6	US-10-857-484-4611	Sequence 4611, Ap	513	17	34.7	9	7	US-11-045-024-12166	Sequence 12166, A
441	17	34.7	9	6	US-10-857-484-4680	Sequence 4680, Ap	514	17	34.7	9	7	US-11-045-024-12608	Sequence 12608, A
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463	17	34.7	9	6	US-10-857-484-5009	Sequence 5009, Ap	536	17	34.7	9	7	US-11-045-024-14374	Sequence 14374, A
					Sequence 5067, Ap								

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538	17	34.7	9	7	US-11-078-256-13	Sequence 13, Appl	611	16	32.7	9	6	US-10-857-484-2057	Sequence 2057, Ap
539	17	34.7	9	7	US-11-078-256-60	Sequence 60, Appl	612	16	32.7	9	6	US-10-857-484-2069	Sequence 2069, Ap
540	17	34.7	9	7	US-11-078-256-61	Sequence 61, Appl	613	16	32.7	9	6	US-10-857-484-2554	Sequence 2554, Ap
541	17	34.7	9	7	US-11-078-256-147	Sequence 147, Appl	614	16	32.7	9	6	US-10-857-484-2567	Sequence 2567, Ap
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546	16	32.7	5	7	US-11-197-038-24	Sequence 24, Appl	619	16	32.7	9	6	US-10-857-484-2637	Sequence 2637, Ap
547	16	32.7	5	7	US-11-249-847-81	Sequence 81, Appl	620	16	32.7	9	6	US-10-857-484-3103	Sequence 3103, Ap
548	16	32.7	6	7	US-11-145-861-290	Sequence 290, Appl	621	16	32.7	9	6	US-10-857-484-3138	Sequence 3138, Ap
549	16	32.7	6	7	US-10-982-891-77	Sequence 77, Appl	622	16	32.7	9	6	US-10-857-484-3141	Sequence 3141, Ap
550	16	32.7	7	6	US-10-467-657-8820	Sequence 8820, Ap	623	16	32.7	9	6	US-10-857-484-3161	Sequence 3161, Ap
551	16	32.7	7	6	US-10-895-064-2517	Sequence 2517, Ap	624	16	32.7	9	6	US-10-857-484-3176	Sequence 3176, Ap
552	16	32.7	7	7	US-11-033-365-59	Sequence 59, Appl	625	16	32.7	9	6	US-10-857-484-3182	Sequence 3182, Ap
553	16	32.7	7	7	US-11-033-365-60	Sequence 60, Appl	626	16	32.7	9	6	US-10-857-484-3673	Sequence 3673, Ap
554	16	32.7	7	7	US-11-064-785-18	Sequence 18, Appl	627	16	32.7	9	6	US-10-857-484-3677	Sequence 3677, Ap
555	16	32.7	7	7	US-11-031-737A-36	Sequence 36, Appl	628	16	32.7	9	6	US-10-857-484-3684	Sequence 3684, Ap
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557	16	32.7	7	7	US-11-225-686-1551	Sequence 1551, Ap	630	16	32.7	9	6	US-10-857-484-3746	Sequence 3746, Ap
558	16	32.7	7	7	US-11-225-686-1555	Sequence 1555, Ap	631	16	32.7	9	6	US-10-857-484-3767	Sequence 3767, Ap
559	16	32.7	7	7	US-11-225-686-3593	Sequence 3593, Ap	632	16	32.7	9	6	US-10-857-484-4147	Sequence 4147, Ap
560	16	32.7	7	7	US-11-225-686-3594	Sequence 3594, Ap	633	16	32.7	9	6	US-10-857-484-4154	Sequence 4154, Ap
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562	16	32.7	7	7	US-11-202-009-1555	Sequence 1555, Ap	635	16	32.7	9	6	US-10-857-484-4437	Sequence 4437, Ap
563	16	32.7	7	7	US-11-202-009-3593	Sequence 3593, Ap	636	16	32.7	9	6	US-10-857-484-4520	Sequence 4520, Ap
564	16	32.7	7	7	US-11-202-009-3594	Sequence 3594, Ap	637	16	32.7	9	6	US-10-857-484-4541	Sequence 4541, Ap
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583	16	32.7	9	6	US-10-989-767A-25	Sequence 25, Appl	656	16	32.7	9	6	US-10-857-484-5103	Sequence 5103, Ap
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585	16	32.7	9	6	US-10-989-767A-110	Sequence 110, Appl	658	16	32.7	9	6	US-10-857-484-5120	Sequence 5120, Ap
586	16	32.7	9	6	US-10-989-767A-204	Sequence 204, Appl	659	16	32.7	9	7	US-11-010-748A-301	Sequence 301, App
587	16	32.7	9	6	US-10-989-767A-210	Sequence 210, Appl	660	16	32.7	9	7	US-11-010-748A-302	Sequence 302, App
588	16	32.7	9	6	US-10-989-767A-218	Sequence 218, Appl	661	16	32.7	9	7	US-11-010-748A-305	Sequence 305, App
589	16	32.7	9	6	US-10-989-767A-483	Sequence 483, Appl	662	16	32.7	9	7	US-11-010-748A-306	Sequence 306, App
590	16	32.7	9	6	US-10-857-484-35	Sequence 35, Appl	663	16	32.7	9	7	US-11-045-024-623	Sequence 623, App
591	16	32.7	9	6	US-10-857-484-282	Sequence 282, Appl	664	16	32.7	9	7	US-11-045-024-2490	Sequence 2490, App
592	16	32.7	9	6	US-10-857-484-317	Sequence 317, Appl	665	16	32.7	9	7	US-11-045-024-2491	Sequence 2491, App
593	16	32.7	9	6	US-10-857-484-333	Sequence 335, Appl	666	16	32.7	9	7	US-11-045-024-3724	Sequence 3724, Ap
594	16	32.7	9	6	US-10-857-484-343	Sequence 343, Appl	667	16	32.7	9	7	US-11-045-024-5417	Sequence 5417, Ap
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597	16	32.7	9	6	US-10-857-484-860	Sequence 860, Appl	670	16	32.7	9	7	US-11-045-024-12196	Sequence 12196, A
598	16	32.7	9	6	US-10-857-484-870	Sequence 870, Appl	671	16	32.7	9	7	US-11-045-024-13954	Sequence 13954, A
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600	16	32.7	9	6	US-10-857-484-936	Sequence 936, Appl	673	16	32.7	9	7	US-11-033-039-451	Sequence 451, App
601	16	32.7	9	6	US-10-857-484-944	Sequence 944, Appl	674	16	32.7	9	7	US-11-033-039-548	Sequence 548, App
602	16	32.7	9	6	US-10-857-484-1430	Sequence 1430, Appl	675	16	32.7	9	7	US-11-033-039-684	Sequence 684, App
603	16	32.7	9	6	US-10-857-484-1440	Sequence 1440, Appl	676	16	32.7	9	7	US-11-033-039-708	Sequence 708, App
604	16	32.7	9	6	US-10-857-484-1442	Sequence 1442, Appl	677	16	32.7	9	7	US-11-041-893-152	Sequence 152, App
605	16	32.7	9	6	US-10-857-484-1483	Sequence 1483, Appl	678	16	32.7	9	7	US-11-104-117-14	Sequence 14, Appl
606	16	32.7	9	6	US-10-857-484-1494	Sequence 1494, Appl	679	16	32.7	9	7	US-11-031-737A-46	Sequence 46, Appl
607	16	32.7	9	6	US-10-857-484-1511	Sequence 1511, Appl	680	16	32.7	9	7	US-11-116-203-78	Sequence 78, Appl
608	16	32.7	9	6	US-10-857-484-1999	Sequence 1999, Appl	681	16	32.7	9	7	US-11-233-253-14	Sequence 14, Appl
609	16	32.7	9	6	US-10-857-484-2001	Sequence 2001, Appl	682	16	32.7	9	7	US-11-233-683-6	Sequence 6, Appl

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684	16	32.7	9	7	US-11-233-683-18	Sequence 18, Appl	757	15	30.6	8	7	US-11-045-024-6007	Sequence 6007, Ap
685	16	32.7	9	7	US-11-031-483-46	Sequence 46, Appl	758	15	30.6	8	7	US-11-045-024-6174	Sequence 6174, Ap
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687	16	32.7	9	7	US-11-129-741-2898	Sequence 2898, Ap	760	15	30.6	8	7	US-11-045-024-6820	Sequence 6820, Ap
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692	15	30.6	5	7	US-11-165-576-72	Sequence 72, Appl	765	15	30.6	8	7	US-11-045-024-7918	Sequence 7918, Ap
693	15	30.6	5	7	US-11-121-613-390	Sequence 390, App	766	15	30.6	8	7	US-11-045-024-7983	Sequence 7983, Ap
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695	15	30.6	5	7	US-11-249-847-214	Sequence 214, App	768	15	30.6	8	7	US-11-045-024-9814	Sequence 9814, Ap
696	15	30.6	5	7	US-11-249-847-254	Sequence 254, App	769	15	30.6	8	7	US-11-045-024-9815	Sequence 9815, Ap
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706	15	30.6	6	6	US-10-857-435A-498	Sequence 498, App	779	15	30.6	8	7	US-11-045-024-14332	Sequence 14332, A
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708	15	30.6	6	6	US-10-857-435A-500	Sequence 500, App	781	15	30.6	8	7	US-11-066-967-120	Sequence 120, App
709	15	30.6	6	6	US-10-857-435A-501	Sequence 501, App	782	15	30.6	8	7	US-11-066-967-133	Sequence 133, App
710	15	30.6	6	6	US-10-857-435A-502	Sequence 502, App	783	15	30.6	8	7	US-11-066-967-133	Sequence 133, App
711	15	30.6	6	6	US-10-857-435A-519	Sequence 519, App	784	15	30.6	8	7	US-11-129-741-1881	Sequence 1881, Ap
712	15	30.6	6	6	US-10-857-435A-523	Sequence 523, App	785	15	30.6	9	6	US-10-997-201A-39	Sequence 39, Appl
713	15	30.6	6	7	US-11-032-773-186	Sequence 186, App	786	15	30.6	9	6	US-10-952-535A-44	Sequence 44, Appl
714	15	30.6	6	7	US-11-234-424-25	Sequence 25, Appl	787	15	30.6	9	6	US-10-491-096-8	Sequence 8, Appli
715	15	30.6	7	6	US-10-842-877A-39	Sequence 39, Appl	788	15	30.6	9	6	US-10-491-096-70	Sequence 70, Appl
716	15	30.6	7	6	US-10-467-033-4	Sequence 4, Appli	789	15	30.6	9	6	US-10-491-096-183	Sequence 183, App
717	15	30.6	7	6	US-10-467-033-10	Sequence 10, Appl	790	15	30.6	9	6	US-10-925-366A-21	Sequence 21, Appl
718	15	30.6	7	6	US-10-467-033-12	Sequence 12, Appl	791	15	30.6	9	6	US-10-956-755A-9	Sequence 9, Appli
719	15	30.6	7	6	US-10-467-033-20	Sequence 20, Appl	792	15	30.6	9	6	US-10-859-643-17	Sequence 17, Appl
720	15	30.6	7	6	US-10-467-033-22	Sequence 22, Appl	793	15	30.6	9	6	US-10-859-643-22	Sequence 22, Appl
721	15	30.6	7	6	US-10-895-064-1781	Sequence 1781, Ap	794	15	30.6	9	6	US-10-859-643-44	Sequence 44, Appl
722	15	30.6	7	6	US-10-895-064-1813	Sequence 1813, Ap	795	15	30.6	9	6	US-10-859-643-114	Sequence 114, App
723	15	30.6	7	7	US-11-069-858-8	Sequence 8, Appli	796	15	30.6	9	6	US-10-859-643-130	Sequence 130, App
724	15	30.6	7	7	US-11-183-664-29	Sequence 29, Appl	797	15	30.6	9	6	US-10-859-643-140	Sequence 140, App
725	15	30.6	7	7	US-11-225-686-3253	Sequence 3253, Ap	798	15	30.6	9	6	US-10-859-643-272	Sequence 272, App
726	15	30.6	7	7	US-11-225-686-3267	Sequence 3267, Ap	799	15	30.6	9	6	US-10-859-643-281	Sequence 281, App
727	15	30.6	7	7	US-11-225-686-3282	Sequence 3282, Ap	800	15	30.6	9	6	US-10-859-643-355	Sequence 355, App
728	15	30.6	7	7	US-11-202-009-3253	Sequence 3253, Ap	801	15	30.6	9	6	US-10-859-643-457	Sequence 457, App
729	15	30.6	7	7	US-11-202-009-3267	Sequence 3267, Ap	802	15	30.6	9	6	US-10-859-643-491	Sequence 491, App
730	15	30.6	7	7	US-11-202-009-3282	Sequence 3282, Ap	803	15	30.6	9	6	US-10-859-643-554	Sequence 554, App
731	15	30.6	7	7	US-11-129-741-1781	Sequence 1781, Ap	804	15	30.6	9	6	US-10-859-643-566	Sequence 566, App
732	15	30.6	7	7	US-11-129-741-1813	Sequence 1813, Ap	805	15	30.6	9	6	US-10-859-643-588	Sequence 588, App
733	15	30.6	7	7	US-11-247-423-229	Sequence 229, App	806	15	30.6	9	6	US-10-859-643-660	Sequence 660, App
734	15	30.6	8	6	US-10-989-226-69	Sequence 69, Appl	807	15	30.6	9	6	US-10-859-643-663	Sequence 663, App
735	15	30.6	8	6	US-10-989-226-77	Sequence 77, Appl	808	15	30.6	9	6	US-10-859-643-697	Sequence 697, App
736	15	30.6	8	6	US-10-989-226-81	Sequence 81, Appl	809	15	30.6	9	6	US-10-895-064-2776	Sequence 2776, Ap
737	15	30.6	8	6	US-10-842-877A-31	Sequence 31, Appl	810	15	30.6	9	6	US-10-989-767A-23	Sequence 23, Appl
738	15	30.6	8	6	US-10-822-246-69	Sequence 69, Appl	811	15	30.6	9	6	US-10-989-767A-37	Sequence 37, Appl
739	15	30.6	8	6	US-10-895-064-1881	Sequence 1881, Ap	812	15	30.6	9	6	US-10-989-767A-44	Sequence 44, Appl
740	15	30.6	8	7	US-11-045-024-463	Sequence 463, App	813	15	30.6	9	6	US-10-989-767A-313	Sequence 313, App
741	15	30.6	8	7	US-11-045-024-1697	Sequence 1697, Ap	814	15	30.6	9	6	US-10-989-767A-475	Sequence 475, App
742	15	30.6	8	7	US-11-045-024-1698	Sequence 1698, Ap	815	15	30.6	9	6	US-10-989-767A-567	Sequence 567, App
743	15	30.6	8	7	US-11-045-024-1730	Sequence 1730, Ap	816	15	30.6	9	6	US-10-989-767A-577	Sequence 577, App
744	15	30.6	8	7	US-11-045-024-2475	Sequence 2475, Ap	817	15	30.6	9	6	US-10-857-484-284	Sequence 284, App
745	15	30.6	8	7	US-11-045-024-3164	Sequence 3164, Ap	818	15	30.6	9	6	US-10-857-484-309	Sequence 309, App
746	15	30.6	8	7	US-11-045-024-3165	Sequence 3165, Ap	819	15	30.6	9	6	US-10-857-484-316	Sequence 316, App
747	15	30.6	8	7	US-11-045-024-4015	Sequence 4015, Ap	820	15	30.6	9	6	US-10-857-484-352	Sequence 352, App
748	15	30.6	8	7	US-11-045-024-4379	Sequence 4379, Ap	821	15	30.6	9	6	US-10-857-484-374	Sequence 374, App
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750	15	30.6	8	7	US-11-045-024-4389	Sequence 4389, Ap	823	15	30.6	9	6	US-10-857-484-890	Sequence 890, App
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837	15	30.6	9	6	US-10-857-484-2019	Sequence 2019, Ap	910	15	30.6	9	7	US-11-097-912-44	Sequence 44, Appl
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982 15 30.6 9 7 US-11-026-403-27 Sequence 27, Appl
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984 15 30.6 9 7 US-11-033-039-702 Sequence 702, App
985 15 30.6 9 7 US-11-033-039-831 Sequence 831, App
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994 15 30.6 9 7 US-11-247-423-188 Sequence 188, App
995 15 30.6 9 7 US-11-247-423-193 Sequence 193, App
996 15 30.6 9 7 US-11-247-423-194 Sequence 194, App
997 15 30.6 9 7 US-11-247-423-265 Sequence 265, App
998 15 30.6 9 7 US-11-247-423-511 Sequence 511, App
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ALIGNMENTS

RESULT 1
US-10-401-386B-52
; Sequence 52, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallan
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; TITLE OF INVENTION: for Use
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
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DB 1 STAPPVHV 9
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US-10-517-784-35
; Sequence 35, Application US/10517784
; Publication No. US2006003315A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro

; APPLICANT: GROSS, Gideon
; APPLICANT: MARGALIT, Alon
; TITLE OF INVENTION: MEMBRANE-ANCHORED BETA-2 MICROGLOBULIN COVALENTLY LINKED TO MHC (PPTIDE EPITOPES
; FILE REFERENCE: GAVISH-004 US
; CURRENT APPLICATION NUMBER: US/10/517,784
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 60/388,273
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/IL03/00501
; PRIOR FILING DATE: 2003-06-12
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-517-784-35
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Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 STAPPVHV 9
DB 1 STAPPVHV 9
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; Sequence 56, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallan
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; TITLE OF INVENTION: for Use
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
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US-10-401-386B-56
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DB 1 STAPPVHV 9
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; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro


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Db          2 TAPPAES 8

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; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cellis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-148

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QY          2 TAPPVHN 8
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; Publication No. US20050271676A1
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; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cellis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
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; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
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; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-148

Query Match          49.0%; Score 24; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 8.3e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY          2 TAPPVHN 8
Db          2 TAPPAES 8

RESULT 12
US-11-045-024-4112
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; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cellis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
```


;; PRIOR APPLICATION NUMBER: US 08/073,205
;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/103,396
;; PRIOR FILING DATE: 1993-08-06
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/159,339
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/347,610
;; PRIOR FILING DATE: 1994-12-01
;; NUMBER OF SEQ ID NOS: 14528
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6287
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6287

Query Match 49.0%; Score 24; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 8.3e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAPPVHN 8
Db 2 TAPPAES 8

RESULT 16
US-11-045-024-6387
;; Sequence 6387, Application US/11045024
;; Publication No. US20050271676A1
;; GENERAL INFORMATION:
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Livingston, Brian
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Baker, Denise Marie
;; APPLICANT: Celis, Esteban
;; APPLICANT: Kubo, Ralph
;; APPLICANT: Grey, Howard M.
;; APPLICANT: Epimmune Inc.
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
;; FILE REFERENCE: 2060, 0040007
;; CURRENT APPLICATION NUMBER: US/11/045,024
;; CURRENT FILING DATE: 2005-01-28
;; PRIOR APPLICATION NUMBER: US 09/412,863
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: US 08/027,146
;; PRIOR FILING DATE: 1993-03-05
;; PRIOR APPLICATION NUMBER: US 08/073,205
;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/103,396
;; PRIOR FILING DATE: 1993-08-06
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/159,339
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/347,610
;; PRIOR FILING DATE: 1994-12-01
;; NUMBER OF SEQ ID NOS: 14528
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6387
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6387

Query Match 49.0%; Score 24; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 8.3e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAPPVHN 8
Db 2 TAPPAES 8

RESULT 17
US-11-045-024-8861
;; Sequence 8861, Application US/11045024
;; Publication No. US20050271676A1
;; GENERAL INFORMATION:
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Livingston, Brian
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Baker, Denise Marie
;; APPLICANT: Celis, Esteban
;; APPLICANT: Kubo, Ralph
;; APPLICANT: Grey, Howard M.
;; APPLICANT: Epimmune Inc.
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
;; FILE REFERENCE: 2060, 0040007
;; CURRENT APPLICATION NUMBER: US/11/045,024
;; CURRENT FILING DATE: 2005-01-28
;; PRIOR APPLICATION NUMBER: US 09/412,863
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: US 08/027,146
;; PRIOR FILING DATE: 1993-03-05
;; PRIOR APPLICATION NUMBER: US 08/073,205
;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/103,396
;; PRIOR FILING DATE: 1993-08-06
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/159,339
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/347,610
;; NUMBER OF SEQ ID NOS: 14528
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8861
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8861

Query Match 49.0%; Score 24; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 8.3e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAPPVHN 8
Db 2 TAPPAES 8

RESULT 18
US-11-045-024-8862
;; Sequence 8862, Application US/11045024
;; Publication No. US20050271676A1
;; GENERAL INFORMATION:
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Livingston, Brian
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Baker, Denise Marie

```

; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8862
; TYPE: PRT
; LENGTH: 9
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8862

Query Match 49.0%; Score 24; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 8.3e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAPPVHN 8
DB 1 TAPPAES 7

RESULT 19
US-11-045-024-9107
; Sequence 9107, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8862
; TYPE: PRT
; LENGTH: 9
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8862

Query Match 49.0%; Score 24; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 8.3e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAPPVHN 8
DB 1 TAPPAES 7

RESULT 19
US-11-045-024-9107
; Sequence 9107, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339

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; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9107
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9107

Query Match 49.0%; Score 24; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 8.3e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAPPVHN 8
DB 2 TAPPAES 8

RESULT 20
US-11-045-024-11134
; Sequence 11134, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11134
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-11134

Query Match 49.0%; Score 24; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 8.3e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAPPVHN 8
DB 1 TAPPAES 7

```

RESULT 21
US-11-031-737A-40
; Sequence 40, Application US/11031737A
; Publication No. US20060019240A1
; GENERAL INFORMATION:
; APPLICANT: Alroy, Iris
; APPLICANT: Greener, Tsvika
; APPLICANT: Tuvia, Shmuel
; APPLICANT: Ben-Avraham, Danny
; TITLE OF INVENTION: POSH NUCLEIC ACIDS, POLYPEPTIDES AND RELATED METHODS
; FILE REFERENCE: PROL-P03-010
; CURRENT APPLICATION NUMBER: US/11/031,737A
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 10/293,965
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/345,846
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/364,530
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence motif
US-11-031-737A-40

Query Match 46.9%; Score 23; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAPP 5
|||
Db 2 TAPP 5

RESULT 22
US-11-031-482-40
; Sequence 40, Application US/11031482
; Publication No. US20060035213A1
; GENERAL INFORMATION:
; APPLICANT: Alroy, Iris
; APPLICANT: Greener, Tsvika
; APPLICANT: Tuvia, Shmuel
; APPLICANT: Ben-Avraham, Danny
; TITLE OF INVENTION: POSH NUCLEIC ACIDS, POLYPEPTIDES AND RELATED METHODS
; FILE REFERENCE: PROL-P02-010
; CURRENT APPLICATION NUMBER: US/11/031,482
; CURRENT FILING DATE: 2005-01-06
; PRIOR APPLICATION NUMBER: 10/293,965
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/345,846
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/364,530
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence motif
US-11-031-482-40

Query Match 46.9%; Score 23; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAPP 5
|||
Db 2 TAPP 5

RESULT 23
US-11-045-024-5300
; Sequence 5300, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5300
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5300

Query Match 46.9%; Score 23; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PVHNV 9
|||
Db 2 PVHGV 6

RESULT 24
US-11-045-024-6267
; Sequence 6267, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
US-11-045-024-6267

```
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6267
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6267

Query Match          46.9%; Score 23; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TAPP 5
DB      1 TAPP 4

RESULT 25
US-11-045-024-6353
; Sequence 6353, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6267
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6353

Query Match          46.9%; Score 23; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TAPP 5
DB      1 TAPP 4

RESULT 26
US-11-045-024-7822
; Sequence 7822, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7822
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7822

Query Match          46.9%; Score 23; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 PVHNV 9
DB      2 PVHGV 6

RESULT 27
US-11-045-024-8826
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```
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7822
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6353

Query Match          46.9%; Score 23; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TAPP 5
DB      1 TAPP 4

RESULT 26
US-11-045-024-7822
; Sequence 7822, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7822
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7822

Query Match          46.9%; Score 23; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 PVHNV 9
DB      2 PVHGV 6

RESULT 27
US-11-045-024-8826
```



```
; APPLICANT: Epimmune Inc.
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT APPLICATION NUMBER: US/10/510,101
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/413,471
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 10/116,118
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide derived from Human Immunodeficiency Virus
US-10-510-101-58
```

```
Query Match 46.9%; Score 23; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 PVHNV 9
    |||
Db 5 PVHGV 9
```

```
RESULT 31
US-10-510-101-59
; Sequence 59, Application US/10510101
; Publication No. US20060018915A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT APPLICATION NUMBER: US/10/510,101
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/413,471
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 10/116,118
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide derived from Human Immunodeficiency Virus
US-10-510-101-59
```

```
Query Match 46.9%; Score 23; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 PVHNV 9
    |||
Db 5 PVHGV 9
```

```
RESULT 32
US-10-510-101-67
; Sequence 67, Application US/10510101
; Publication No. US20060018915A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT APPLICATION NUMBER: US/10/510,101
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/413,471
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 10/116,118
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide derived from Human Immunodeficiency Virus
US-10-510-101-67
```

```
Query Match 46.9%; Score 23; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 PVHNV 9
    |||
Db 5 PVHGV 9
```

```
RESULT 33
US-10-510-101-83
; Sequence 83, Application US/10510101
; Publication No. US20060018915A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT APPLICATION NUMBER: US/10/510,101
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/413,471
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 10/116,118
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide derived from Homo sapiens melanoma antigens
US-10-510-101-83
```

```
Query Match 46.9%; Score 23; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 8.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 PPVH 7
    ||:|
Db 4 PPLH 7
```

```
RESULT 34
US-10-510-101-175
; Sequence 175, Application US/10510101
```

Publication No. US20060018915A1
GENERAL INFORMATION:
APPLICANT: Epimmune Inc.
APPLICANT: Ishioka, Glenn
APPLICANT: Fikes, John
APPLICANT: Tangri, Shabnam
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
FILE REFERENCE: 2060.009PC05
CURRENT APPLICATION NUMBER: US/10/510,101
CURRENT FILING DATE: 2004-10-05
PRIOR APPLICATION NUMBER: US 60/413,471
PRIOR FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 10/116,118
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn version 3.2
SEQ ID NO 175
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide derived from Homo sapiens melanoma antigens
US-10-510-101-175

Query Match 46.9%; Score 23; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 8.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPVH 7
DB 4 PPLH 7

RESULT 35
US-11-045-024-147
Sequence 147, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 147

LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-147

Query Match 46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAPP 5
DB 2 TAPP 5

RESULT 36
US-11-045-024-149
Sequence 149, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 149
LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-149

Query Match 46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAPP 5
DB 2 TAPP 5

RESULT 37
US-11-045-024-1247
Sequence 1247, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro

```

; APPLICANT: Sidney,John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1247
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1247

Query Match 46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAPP 5
DB 5 TAPP 8

RESULT 38
US-11-045-024-1885
; Sequence 1885, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Esteban
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1247
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1247

```

```

; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1885
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1885

Query Match 46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PVHNV 9
DB 5 PVHGV 9

RESULT 39
US-11-045-024-2987
; Sequence 2987, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2987
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2987

Query Match 46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4115
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4115

Query Match          46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 TAPP 5
Db   2 TAPP 5

RESULT 43
US-11-045-024-5192
; Sequence 5192, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5195
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5195

Query Match          46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 TAPP 5
Db   5 TAPP 8

RESULT 45
US-11-045-024-5845
; Sequence 5845, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
```

```
RESULT 44
US-11-045-024-5195
; Sequence 5195, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5195
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5195

Query Match          46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 TAPP 5
Db   5 TAPP 8

RESULT 45
US-11-045-024-5845
; Sequence 5845, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
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; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5845
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5845

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Query Match      46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      5 PVHNV 9
Db      4 PVHGV 8

```

```

RESULT 46
US-11-045-024-6269
; Sequence 6269, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cellis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6269
; LENGTH: 9

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; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6269

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```

Query Match      46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 TAPP 5
Db      2 TAPP 5

```

```

RESULT 47
US-11-045-024-6358
; Sequence 6358, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cellis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6358
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6358

```

```

Query Match      46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      2 TAPP 5
Db      2 TAPP 5

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```

RESULT 48
US-11-045-024-7824
; Sequence 7824, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John

```

```

; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7824
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7824

Query Match 46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PVHNV 9
Db 5 PVHGV 9

RESULT 49
US-11-045-024-8253
; Sequence 8253, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8253
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8253

Query Match 46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PVHNV 9
Db 5 PVHGV 9

RESULT 49
US-11-045-024-8253
; Sequence 8253, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8253
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8253

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; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8253
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8253

Query Match 46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PVHNV 9
Db 4 PVHGV 8

RESULT 50
US-11-045-024-8830
; Sequence 8830, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8830
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8830

Query Match 46.9%; Score 23; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 TAPP 5
Db 2 TAPP 5

Search completed: February 24, 2006, 10:32:45
Job time : 23 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 24, 2006, 10:29:20 ; Search time 161 Seconds
(without alignments)
23.357 Million cell updates/sec

Title: US-10-019-513-1
Perfect score: 49
Sequence: 1 STAPPVHVNV

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 180914

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	9	4	US-10-447-161-98
2	39	79.6	9	3	US-09-903-460-55
3	39	79.6	9	3	US-09-872-836-55
4	39	79.6	9	4	US-10-447-161-97
5	39	79.6	9	4	US-10-296-317-44
6	39	79.6	9	5	US-10-758-970-55
7	39	79.6	9	5	US-10-751-845-9
8	37	75.5	8	5	US-10-973-927-19
9	32	65.3	8	3	US-09-994-466-10
10	31.5	64.3	8	4	US-10-080-013-20
11	31.5	64.3	8	4	US-10-289-566-20
12	31	63.3	6	3	US-09-994-466-7
13	31	63.3	9	6	US-11-055-119-3
14	28	57.1	9	4	US-10-334-726-100
15	27	55.1	9	3	US-09-077-214-28
16	27	55.1	9	6	US-11-055-119-9
17	26	53.1	8	5	US-10-473-137-175
18	25	51.0	9	3	US-09-879-936-22
19	25	51.0	9	4	US-10-001-546-67
20	25	51.0	9	4	US-10-182-252A-170
21	25	51.0	9	4	US-10-182-252A-172
22	25	51.0	9	4	US-10-611-440-14
23	24	49.0	7	3	US-09-954-385-198
24	24	49.0	7	5	US-10-912-512-198
25	24	49.0	7	5	US-10-233-043-198
26	24	49.0	8	4	US-10-786-850-33
27	24	49.0	8	6	US-11-051-411-80

28	24	49.0	8	6	US-11-051-411-107	Sequence 107, App
29	24	49.0	8	6	US-11-051-411-287	Sequence 287, App
30	24	49.0	8	6	US-11-051-411-496	Sequence 496, App
31	24	49.0	8	6	US-11-051-411-667	Sequence 667, App
32	24	49.0	8	6	US-11-051-411-887	Sequence 887, App
33	24	49.0	9	3	US-09-932-369A-5	Sequence 5, Appl
34	24	49.0	9	3	US-09-833-203-38	Sequence 38, Appl
35	24	49.0	9	4	US-10-809-790-7	Sequence 7, Appl
36	24	49.0	9	5	US-10-862-195-1350	Sequence 1350, App
37	24	49.0	9	6	US-11-051-411-81	Sequence 81, Appl
38	24	49.0	9	6	US-11-051-411-219	Sequence 219, App
39	24	49.0	9	6	US-11-051-411-288	Sequence 288, App
40	24	49.0	9	6	US-11-051-411-368	Sequence 368, App
41	24	49.0	9	6	US-11-051-411-544	Sequence 544, App
42	24	49.0	9	6	US-11-051-411-557	Sequence 557, App
43	24	49.0	9	6	US-11-051-411-733	Sequence 733, App
44	24	49.0	9	6	US-11-051-411-817	Sequence 817, App
45	24	49.0	9	6	US-11-051-411-939	Sequence 939, App
46	24	49.0	9	6	US-11-051-411-998	Sequence 998, App
47	23	46.9	5	3	US-09-972-035A-9	Sequence 9, Appl
48	23	46.9	5	4	US-10-223-172A-9	Sequence 9, Appl
49	23	46.9	5	4	US-10-224-999A-9	Sequence 9, Appl
50	23	46.9	5	4	US-10-663-407-9	Sequence 9, Appl
51	23	46.9	6	3	US-09-972-035A-11	Sequence 11, Appl
52	23	46.9	6	3	US-09-978-244A-67	Sequence 67, Appl
53	23	46.9	6	4	US-10-223-172A-11	Sequence 11, Appl
54	23	46.9	6	4	US-10-224-999A-11	Sequence 11, Appl
55	23	46.9	6	4	US-10-663-407-11	Sequence 11, Appl
56	23	46.9	7	3	US-09-192-854-91	Sequence 91, Appl
57	23	46.9	7	3	US-09-968-561A-159	Sequence 159, App
58	23	46.9	7	3	US-09-972-035A-17	Sequence 17, Appl
59	23	46.9	7	3	US-09-968-744A-159	Sequence 159, App
60	23	46.9	7	3	US-09-968-561A-159	Sequence 159, App
61	23	46.9	7	4	US-10-097-534-67	Sequence 67, Appl
62	23	46.9	7	4	US-10-097-534-68	Sequence 68, Appl
63	23	46.9	7	4	US-10-223-172A-17	Sequence 17, Appl
64	23	46.9	7	4	US-10-224-999A-17	Sequence 17, Appl
65	23	46.9	7	4	US-10-299-991-6	Sequence 6, Appl
66	23	46.9	7	4	US-10-299-991-7	Sequence 7, Appl
67	23	46.9	7	4	US-10-663-407-17	Sequence 17, Appl
68	23	46.9	7	5	US-10-935-642-81	Sequence 81, Appl
69	23	46.9	7	5	US-10-485-225-97	Sequence 97, Appl
70	23	46.9	7	5	US-10-485-225-98	Sequence 98, Appl
71	23	46.9	7	6	US-11-115-682-159	Sequence 159, App
72	23	46.9	7	6	US-11-074-473-81	Sequence 81, Appl
73	23	46.9	8	3	US-09-117-380B-13	Sequence 13, Appl
74	23	46.9	8	3	US-09-117-380B-20	Sequence 20, Appl
75	23	46.9	8	3	US-09-972-035A-19	Sequence 19, Appl
76	23	46.9	8	3	US-09-972-035A-21	Sequence 21, Appl
77	23	46.9	8	4	US-10-185-815-76	Sequence 76, Appl
78	23	46.9	8	4	US-10-133-210-199	Sequence 199, App
79	23	46.9	8	4	US-10-226-007-65	Sequence 65, Appl
80	23	46.9	8	4	US-10-226-007-78	Sequence 78, Appl
81	23	46.9	8	4	US-10-226-007-91	Sequence 91, Appl
82	23	46.9	8	4	US-10-223-172A-19	Sequence 19, Appl
83	23	46.9	8	4	US-10-223-172A-21	Sequence 21, Appl
84	23	46.9	8	4	US-10-224-999A-19	Sequence 19, Appl
85	23	46.9	8	4	US-10-224-999A-21	Sequence 21, Appl
86	23	46.9	8	4	US-10-224-999A-39	Sequence 39, Appl
87	23	46.9	8	4	US-10-224-999A-40	Sequence 40, Appl
88	23	46.9	8	4	US-10-224-999A-41	Sequence 41, Appl
89	23	46.9	8	4	US-10-224-999A-42	Sequence 42, Appl
90	23	46.9	8	4	US-10-224-999A-127	Sequence 127, App
91	23	46.9	8	4	US-10-224-999A-128	Sequence 128, App
92	23	46.9	8	4	US-10-224-999A-129	Sequence 129, App
93	23	46.9	8	4	US-10-224-999A-130	Sequence 130, App
94	23	46.9	8	4	US-10-224-999A-269	Sequence 269, App
95	23	46.9	8	4	US-10-224-999A-270	Sequence 270, App
96	23	46.9	8	4	US-10-224-999A-556	Sequence 556, App
97	23	46.9	8	4	US-10-224-999A-557	Sequence 557, App
98	23	46.9	8	4	US-10-224-999A-558	Sequence 558, App
99	23	46.9	8	4	US-10-224-999A-559	Sequence 559, App
100	23	46.9	8	4	US-10-239-313A-173	Sequence 173, App

101	23	46.9	8	4	US-10-116-275-89	Sequence 89, Appl	174	23	46.9	9	4	US-10-223-172A-22	Sequence 22, Appl
102	23	46.9	8	4	US-10-149-135-762	Sequence 762, App	175	23	46.9	9	4	US-10-223-172A-23	Sequence 23, Appl
103	23	46.9	8	4	US-10-149-135-802	Sequence 802, App	176	23	46.9	9	4	US-10-223-172A-25	Sequence 25, Appl
104	23	46.9	8	4	US-10-149-135-811	Sequence 811, App	177	23	46.9	9	4	US-10-223-172A-26	Sequence 26, Appl
105	23	46.9	8	4	US-10-149-135-841	Sequence 841, App	178	23	46.9	9	4	US-10-079-167-61	Sequence 61, Appl
106	23	46.9	8	4	US-10-149-135-849	Sequence 849, App	179	23	46.9	9	4	US-10-266-463A-42	Sequence 42, Appl
107	23	46.9	8	4	US-10-149-135-1283	Sequence 1283, Ap	180	23	46.9	9	4	US-10-266-463A-48	Sequence 48, Appl
108	23	46.9	8	4	US-10-149-135-1287	Sequence 1287, Ap	181	23	46.9	9	4	US-10-116-118-18	Sequence 18, Appl
109	23	46.9	8	4	US-10-149-135-1362	Sequence 1362, Ap	182	23	46.9	9	4	US-10-116-118-19	Sequence 19, Appl
110	23	46.9	8	4	US-10-149-135-1706	Sequence 1562, Ap	183	23	46.9	9	4	US-10-116-118-20	Sequence 20, Appl
111	23	46.9	8	4	US-10-149-135-1806	Sequence 1806, Ap	184	23	46.9	9	4	US-10-283-847-15	Sequence 15, Appl
112	23	46.9	8	4	US-10-149-135-1808	Sequence 1808, Ap	185	23	46.9	9	4	US-10-224-999A-22	Sequence 22, Appl
113	23	46.9	8	4	US-10-149-135-1908	Sequence 1908, Ap	186	23	46.9	9	4	US-10-224-999A-23	Sequence 23, Appl
114	23	46.9	8	4	US-10-149-135-2252	Sequence 2252, Ap	187	23	46.9	9	4	US-10-224-999A-25	Sequence 25, Appl
115	23	46.9	8	4	US-10-663-407-19	Sequence 19, Appl	188	23	46.9	9	4	US-10-224-999A-26	Sequence 26, Appl
116	23	46.9	8	4	US-10-663-407-21	Sequence 21, Appl	189	23	46.9	9	4	US-10-224-999A-44	Sequence 44, Appl
117	23	46.9	8	4	US-10-657-022-337	Sequence 337, App	190	23	46.9	9	4	US-10-224-999A-45	Sequence 45, Appl
118	23	46.9	8	4	US-10-657-022-346	Sequence 346, App	191	23	46.9	9	4	US-10-224-999A-46	Sequence 46, Appl
119	23	46.9	8	6	US-11-147-083-76	Sequence 348, App	192	23	46.9	9	4	US-10-224-999A-47	Sequence 47, Appl
120	23	46.9	9	2	US-08-600-483-2	Sequence 76, Appl	193	23	46.9	9	4	US-10-224-999A-48	Sequence 48, Appl
121	23	46.9	9	2	US-08-344-824-21	Sequence 21, Appl	194	23	46.9	9	4	US-10-224-999A-132	Sequence 132, App
122	23	46.9	9	2	US-08-344-824-149	Sequence 149, App	195	23	46.9	9	4	US-10-224-999A-133	Sequence 133, App
123	23	46.9	9	2	US-08-344-824-156	Sequence 156, App	196	23	46.9	9	4	US-10-224-999A-134	Sequence 134, App
124	23	46.9	9	2	US-08-344-824-339	Sequence 339, App	197	23	46.9	9	4	US-10-224-999A-135	Sequence 135, App
125	23	46.9	9	3	US-09-780-053-464	Sequence 464, App	198	23	46.9	9	4	US-10-224-999A-136	Sequence 136, App
126	23	46.9	9	3	US-09-894-018-6	Sequence 6, Appl	199	23	46.9	9	4	US-10-224-999A-274	Sequence 274, App
127	23	46.9	9	3	US-09-894-018-71	Sequence 71, Appl	200	23	46.9	9	4	US-10-224-999A-275	Sequence 275, App
128	23	46.9	9	3	US-09-894-018-148	Sequence 148, App	201	23	46.9	9	4	US-10-224-999A-276	Sequence 276, App
129	23	46.9	9	3	US-09-912-787-81	Sequence 81, Appl	202	23	46.9	9	4	US-10-224-999A-561	Sequence 561, App
130	23	46.9	9	3	US-09-117-380B-10	Sequence 10, Appl	203	23	46.9	9	4	US-10-224-999A-562	Sequence 562, App
131	23	46.9	9	3	US-09-117-380B-14	Sequence 14, Appl	204	23	46.9	9	4	US-10-224-999A-563	Sequence 563, App
132	23	46.9	9	3	US-09-117-380B-18	Sequence 18, Appl	205	23	46.9	9	4	US-10-224-999A-564	Sequence 564, App
133	23	46.9	9	3	US-09-972-035A-22	Sequence 22, Appl	206	23	46.9	9	4	US-10-224-999A-565	Sequence 565, App
134	23	46.9	9	3	US-09-972-035A-23	Sequence 23, Appl	207	23	46.9	9	4	US-10-224-999A-2756	Sequence 2756, Ap
135	23	46.9	9	3	US-09-277-074-5	Sequence 5, Appl	208	23	46.9	9	4	US-10-200-708-10	Sequence 10, Appl
136	23	46.9	9	3	US-09-277-064-5	Sequence 5, Appl	209	23	46.9	9	4	US-10-200-708-652	Sequence 652, App
137	23	46.9	9	3	US-09-938-864-176	Sequence 176, App	210	23	46.9	9	4	US-10-195-835-176	Sequence 176, App
138	23	46.9	9	3	US-09-938-864-218	Sequence 218, App	211	23	46.9	9	4	US-10-195-835-218	Sequence 218, App
139	23	46.9	9	3	US-09-938-864-292	Sequence 292, App	212	23	46.9	9	4	US-10-195-835-292	Sequence 292, App
140	23	46.9	9	3	US-09-791-477-176	Sequence 176, App	213	23	46.9	9	4	US-10-371-525-101	Sequence 101, App
141	23	46.9	9	3	US-09-791-477-218	Sequence 218, App	214	23	46.9	9	4	US-10-334-726-230	Sequence 230, App
142	23	46.9	9	3	US-09-791-477-292	Sequence 292, App	215	23	46.9	9	4	US-10-286-333-176	Sequence 176, App
143	23	46.9	9	3	US-09-785-019-176	Sequence 176, App	216	23	46.9	9	4	US-10-286-333-218	Sequence 218, App
144	23	46.9	9	3	US-09-785-019-218	Sequence 218, App	217	23	46.9	9	4	US-10-286-333-292	Sequence 292, App
145	23	46.9	9	3	US-09-785-019-292	Sequence 292, App	218	23	46.9	9	4	US-10-371-069-101	Sequence 101, App
146	23	46.9	9	3	US-09-788-110A-7	Sequence 7, Appl	219	23	46.9	9	4	US-10-371-645-101	Sequence 101, App
147	23	46.9	9	4	US-10-014-326-83	Sequence 83, Appl	220	23	46.9	9	4	US-10-371-260-101	Sequence 101, App
148	23	46.9	9	4	US-10-106-487-23	Sequence 23, Appl	221	23	46.9	9	4	US-10-244-830-176	Sequence 176, App
149	23	46.9	9	4	US-10-106-487-32	Sequence 32, Appl	222	23	46.9	9	4	US-10-244-830-218	Sequence 218, App
150	23	46.9	9	4	US-10-125-635A-176	Sequence 176, App	223	23	46.9	9	4	US-10-244-830-292	Sequence 292, App
151	23	46.9	9	4	US-10-125-635A-218	Sequence 218, App	224	23	46.9	9	4	US-10-353-678-23	Sequence 23, Appl
152	23	46.9	9	4	US-10-125-635A-292	Sequence 292, App	225	23	46.9	9	4	US-10-427-717-176	Sequence 176, App
153	23	46.9	9	4	US-10-105-200A-42	Sequence 42, Appl	226	23	46.9	9	4	US-10-427-717-218	Sequence 218, App
154	23	46.9	9	4	US-10-214-524-18	Sequence 18, Appl	227	23	46.9	9	4	US-10-427-717-292	Sequence 292, App
155	23	46.9	9	4	US-10-105-504A-42	Sequence 42, Appl	228	23	46.9	9	4	US-10-448-521-44	Sequence 44, Appl
156	23	46.9	9	4	US-10-105-678A-42	Sequence 42, Appl	229	23	46.9	9	4	US-10-388-337-23	Sequence 23, Appl
157	23	46.9	9	4	US-10-002-603A-176	Sequence 176, App	230	23	46.9	9	4	US-10-388-104-36	Sequence 36, Appl
158	23	46.9	9	4	US-10-002-603A-218	Sequence 218, App	231	23	46.9	9	4	US-10-149-135-54	Sequence 54, Appl
159	23	46.9	9	4	US-10-002-603-292	Sequence 292, App	232	23	46.9	9	4	US-10-149-135-475	Sequence 475, App
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161	23	46.9	9	4	US-10-128-711-76	Sequence 76, Appl	234	23	46.9	9	4	US-10-149-135-850	Sequence 850, App
162	23	46.9	9	4	US-10-114-823B-23	Sequence 23, Appl	235	23	46.9	9	4	US-10-149-135-1028	Sequence 1028, Ap
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164	23	46.9	9	4	US-10-133-210-27	Sequence 27, Appl	237	23	46.9	9	4	US-10-149-135-1713	Sequence 1713, Ap
165	23	46.9	9	4	US-10-133-210-220	Sequence 220, App	238	23	46.9	9	4	US-10-149-135-2051	Sequence 2051, Ap
166	23	46.9	9	4	US-10-133-210-235	Sequence 235, App	239	23	46.9	9	4	US-10-149-135-2115	Sequence 2115, Ap
167	23	46.9	9	4	US-10-226-007-66	Sequence 66, Appl	240	23	46.9	9	4	US-10-149-135-2248	Sequence 2248, Ap
168	23	46.9	9	4	US-10-226-007-79	Sequence 79, Appl	241	23	46.9	9	4	US-10-149-135-2249	Sequence 2249, Ap
169	23	46.9	9	4	US-10-226-007-92	Sequence 92, Appl	242	23	46.9	9	4	US-10-367-580-119	Sequence 119, App
170	23	46.9	9	4	US-10-226-007-104	Sequence 104, App	243	23	46.9	9	4	US-10-367-593-119	Sequence 119, App
171	23	46.9	9	4	US-10-168-843A-21	Sequence 21, Appl	244	23	46.9	9	4	US-10-367-594-119	Sequence 119, App
172	23	46.9	9	4	US-10-219-850-17	Sequence 17, Appl	245	23	46.9	9	4	US-10-367-654-119	Sequence 119, App
173	23	46.9	9	4	US-10-147-910-7	Sequence 7, Appl	246	23	46.9	9	4	US-10-367-658-119	Sequence 119, App

247	23	46.9	9	4	US-10-367-668-119	Sequence 119, App	320	22	44.9	7	4	US-10-609-217-296	Sequence 296, App
248	23	46.9	9	4	US-10-182-252A-64	Sequence 64, App1	321	22	44.9	7	4	US-10-632-388-296	Sequence 296, App
249	23	46.9	9	4	US-10-182-252A-65	Sequence 65, App1	322	22	44.9	7	4	US-10-651-723-296	Sequence 296, App
250	23	46.9	9	4	US-10-182-252A-66	Sequence 66, App1	323	22	44.9	7	4	US-10-645-761-296	Sequence 296, App
251	23	46.9	9	4	US-10-182-252A-68	Sequence 68, App1	324	22	44.9	7	4	US-10-666-696-296	Sequence 296, App
252	23	46.9	9	4	US-10-182-252A-69	Sequence 69, App1	325	22	44.9	7	4	US-10-653-048-296	Sequence 296, App
253	23	46.9	9	4	US-10-182-252A-71	Sequence 71, App1	326	22	44.9	7	4	US-10-807-856-203	Sequence 203, App
254	23	46.9	9	4	US-10-182-252A-74	Sequence 74, App1	327	22	44.9	7	4	US-10-645-784-296	Sequence 296, App
255	23	46.9	9	4	US-10-182-252A-77	Sequence 77, App1	328	22	44.9	7	5	US-10-952-557-280	Sequence 280, App
256	23	46.9	9	4	US-10-182-252A-78	Sequence 78, App1	329	22	44.9	8	4	US-10-952-557-280	Sequence 280, App
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262	23	46.9	9	4	US-10-333-430-45	Sequence 40, App1	334	22	44.9	8	4	US-10-149-138-2028	Sequence 2028, App
263	23	46.9	9	4	US-10-663-407-22	Sequence 45, App1	335	22	44.9	8	5	US-10-862-195-422	Sequence 422, App
264	23	46.9	9	4	US-10-663-407-23	Sequence 22, App1	336	22	44.9	8	6	US-11-051-411-41	Sequence 41, App1
265	23	46.9	9	4	US-10-648-780-176	Sequence 23, App1	337	22	44.9	8	6	US-11-051-411-426	Sequence 256, App
266	23	46.9	9	4	US-10-648-780-218	Sequence 176, App	338	22	44.9	8	6	US-11-051-411-390	Sequence 390, App
267	23	46.9	9	4	US-10-648-780-232	Sequence 218, App	339	22	44.9	8	6	US-11-051-411-578	Sequence 578, App
268	23	46.9	9	4	US-10-367-674-119	Sequence 292, App	340	22	44.9	8	6	US-11-051-411-642	Sequence 642, App
269	23	46.9	9	4	US-10-653-624-61	Sequence 119, App	341	22	44.9	8	6	US-11-051-411-833	Sequence 833, App
270	23	46.9	9	4	US-10-777-053-115	Sequence 61, App1	342	22	44.9	8	6	US-11-051-411-1011	Sequence 1011, App
271	23	46.9	9	4	US-10-777-053-140	Sequence 115, App	343	22	44.9	8	6	US-11-051-411-1233	Sequence 1233, App
272	23	46.9	9	4	US-10-777-053-416	Sequence 140, App	344	22	44.9	8	6	US-11-051-411-1319	Sequence 1319, App
273	23	46.9	9	4	US-10-777-053-748	Sequence 416, App	345	22	44.9	8	6	US-11-051-411-1411	Sequence 1411, App
274	23	46.9	9	4	US-10-777-053-968	Sequence 748, App	346	22	44.9	8	6	US-11-051-411-1411	Sequence 1411, App
275	23	46.9	9	4	US-10-833-439-61	Sequence 968, App	347	22	44.9	9	3	US-09-077-214-31	Sequence 31, App1
276	23	46.9	9	4	US-10-715-417-11	Sequence 61, App1	348	22	44.9	9	3	US-09-758-128-39	Sequence 39, App1
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279	23	46.9	9	4	US-10-657-022-340	Sequence 338, App	351	22	44.9	9	3	US-09-909-460-69	Sequence 69, App1
280	23	46.9	9	4	US-10-657-022-347	Sequence 340, App	352	22	44.9	9	3	US-09-758-198-39	Sequence 39, App1
281	23	46.9	9	4	US-10-657-022-349	Sequence 347, App	353	22	44.9	9	3	US-09-758-198-39	Sequence 39, App1
282	23	46.9	9	4	US-10-833-745-61	Sequence 349, App	354	22	44.9	9	3	US-09-277-074-2	Sequence 2, App1
283	23	46.9	9	4	US-10-833-744-61	Sequence 61, App1	355	22	44.9	9	3	US-09-277-074-3	Sequence 3, App1
284	23	46.9	9	4	US-10-837-217-115	Sequence 61, App1	356	22	44.9	9	3	US-09-861-661-39	Sequence 39, App1
285	23	46.9	9	4	US-10-837-217-140	Sequence 115, App	357	22	44.9	9	3	US-09-277-064-3	Sequence 3, App1
286	23	46.9	9	4	US-10-837-217-416	Sequence 140, App	358	22	44.9	9	3	US-09-872-836-66	Sequence 66, App1
287	23	46.9	9	4	US-10-837-217-748	Sequence 416, App	359	22	44.9	9	3	US-09-872-836-69	Sequence 69, App1
288	23	46.9	9	4	US-10-837-217-968	Sequence 748, App	360	22	44.9	9	4	US-10-106-487-15	Sequence 15, App1
289	23	46.9	9	4	US-10-354-090-11	Sequence 968, App	361	22	44.9	9	4	US-10-106-487-16	Sequence 16, App1
290	23	46.9	9	4	US-10-686-943-61	Sequence 11, App1	362	22	44.9	9	4	US-10-210-148-61	Sequence 61, App1
291	23	46.9	9	5	US-10-769-991-1	Sequence 61, App1	363	22	44.9	9	4	US-10-287-941-10	Sequence 10, App1
292	23	46.9	9	5	US-10-474-960A-6	Sequence 1, App1	364	22	44.9	9	4	US-10-057-475B-10758	Sequence 10758, A
293	23	46.9	9	5	US-10-474-960A-71	Sequence 71, App1	365	22	44.9	9	4	US-10-057-475B-10791	Sequence 10791, A
294	23	46.9	9	5	US-10-474-960A-148	Sequence 148, App	366	22	44.9	9	4	US-10-465-811-84	Sequence 84, App1
295	23	46.9	9	5	US-10-884-862-37	Sequence 37, App1	367	22	44.9	9	4	US-10-465-811-85	Sequence 85, App1
296	23	46.9	9	5	US-10-948-707-475	Sequence 475, App	368	22	44.9	9	4	US-10-154-884B-10758	Sequence 10758, A
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298	23	46.9	9	5	US-10-820-067A-402	Sequence 402, App	370	22	44.9	9	4	US-10-388-337-15	Sequence 15, App1
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300	23	46.9	9	5	US-10-999-364-81	Sequence 574, App	372	22	44.9	9	4	US-10-149-138-584	Sequence 584, App
301	23	46.9	9	5	US-10-953-769-13	Sequence 81, App1	373	22	44.9	9	4	US-10-149-138-2926	Sequence 2926, App
302	23	46.9	9	5	US-11-055-119-66	Sequence 13, App1	374	22	44.9	9	4	US-10-363-791-120	Sequence 120, App
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304	23	46.9	9	6	US-11-005-750-42	Sequence 42, App1	376	22	44.9	9	4	US-10-182-252A-70	Sequence 70, App1
305	23	46.9	9	6	US-11-005-750-48	Sequence 48, App1	377	22	44.9	9	4	US-10-182-252A-73	Sequence 73, App1
306	23	46.9	9	6	US-11-008-958-5	Sequence 5, App1	378	22	44.9	9	4	US-10-182-252A-1179	Sequence 1179, App
307	23	46.9	9	6	US-09-911-838-76	Sequence 23, App1	379	22	44.9	9	4	US-10-149-138-584	Sequence 584, App
308	22	44.9	6	3	US-09-911-838-76	Sequence 76, App1	380	22	44.9	9	4	US-10-149-138-2926	Sequence 2926, App
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312	22	44.9	7	3	US-09-878-957-203	Sequence 203, App	384	22	44.9	9	5	US-10-751-845-20	Sequence 20, App1
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314	22	44.9	7	3	US-09-911-838-77	Sequence 77, App1	386	22	44.9	9	5	US-10-498-468A-5	Sequence 5, App1
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319	22	44.9	7	3	US-10-394-980-280	Sequence 5, App1	391	22	44.9	9	6	US-11-051-411-369	Sequence 369, App
	22	44.9	7	4		Sequence 280, App	392	22	44.9	9	6	US-11-051-411-391	Sequence 391, App

393	22	44.9	9	6	US-11-051-411-530	Sequence 530, App	466	21	42.9	9	4	US-10-001-469-854	Sequence 854, App
394	22	44.9	9	6	US-11-051-411-530	Sequence 597, App	467	21	42.9	9	4	US-10-001-469-1036	Sequence 1036, App
395	22	44.9	9	6	US-11-051-411-671	Sequence 671, App	468	21	42.9	9	4	US-10-001-469-1043	Sequence 1043, App
396	22	44.9	9	6	US-11-051-411-673	Sequence 673, App	469	21	42.9	9	4	US-10-001-469-1221	Sequence 1221, App
397	22	44.9	9	6	US-11-051-411-891	Sequence 891, App	470	21	42.9	9	4	US-10-001-469-1224	Sequence 1224, App
398	22	44.9	9	6	US-11-051-411-1126	Sequence 1126, App	471	21	42.9	9	4	US-10-001-469-1298	Sequence 1298, App
399	22	44.9	9	6	US-11-051-411-1153	Sequence 1153, App	472	21	42.9	9	4	US-10-001-469-1433	Sequence 1433, App
400	22	44.9	9	6	US-11-051-411-1154	Sequence 1154, App	473	21	42.9	9	4	US-10-001-469-1437	Sequence 1437, App
401	22	44.9	9	6	US-11-051-411-1169	Sequence 1169, App	474	21	42.9	9	4	US-10-001-469-1494	Sequence 1494, App
402	22	44.9	9	6	US-11-051-411-1181	Sequence 1181, App	475	21	42.9	9	4	US-10-001-469-1497	Sequence 1497, App
403	22	44.9	9	6	US-11-051-411-1228	Sequence 1228, App	476	21	42.9	9	4	US-10-001-469-1537	Sequence 1537, App
404	22	44.9	9	6	US-11-051-411-1229	Sequence 1229, App	477	21	42.9	9	4	US-10-001-469-1649	Sequence 1649, App
405	22	44.9	9	6	US-11-051-411-1255	Sequence 1255, App	478	21	42.9	9	4	US-10-001-469-1671	Sequence 1671, App
406	22	44.9	9	6	US-11-051-411-1331	Sequence 1331, App	479	21	42.9	9	4	US-10-001-469-1722	Sequence 1722, App
407	22	44.9	9	6	US-11-051-411-1399	Sequence 1399, App	480	21	42.9	9	4	US-10-001-469-1738	Sequence 1738, App
408	22	44.9	9	6	US-11-051-411-1431	Sequence 1431, App	481	21	42.9	9	4	US-10-001-469-1755	Sequence 1755, App
409	22	44.9	9	6	US-11-051-411-1454	Sequence 1454, App	482	21	42.9	9	4	US-10-001-469-1812	Sequence 1812, App
410	21	42.9	4	5	US-10-478-521-61	Sequence 61, Appl	483	21	42.9	9	4	US-10-001-469-2005	Sequence 2005, App
411	21	42.9	6	2	US-08-831-310-11	Sequence 11, Appl	484	21	42.9	9	4	US-10-001-469-2073	Sequence 2073, App
412	21	42.9	6	4	US-10-039-183A-11	Sequence 11, Appl	485	21	42.9	9	4	US-10-001-469-2082	Sequence 2082, App
413	21	42.9	7	5	US-10-808-187-1987	Sequence 1987, App	486	21	42.9	9	4	US-10-001-469-2097	Sequence 2097, App
414	21	42.9	7	5	US-10-807-807-1987	Sequence 1987, App	487	21	42.9	9	4	US-10-002-603-156	Sequence 156, App
415	21	42.9	8	4	US-10-357-929A-7	Sequence 7, Appl	488	21	42.9	9	4	US-10-002-603-157	Sequence 157, App
416	21	42.9	8	4	US-10-367-580-247	Sequence 247, App	489	21	42.9	9	4	US-10-002-603-158	Sequence 158, App
417	21	42.9	8	4	US-10-367-593-247	Sequence 247, App	490	21	42.9	9	4	US-10-002-603-171	Sequence 171, App
418	21	42.9	8	4	US-10-367-594-247	Sequence 247, App	491	21	42.9	9	4	US-10-002-603-290	Sequence 290, App
419	21	42.9	8	4	US-10-367-654-247	Sequence 247, App	492	21	42.9	9	4	US-10-322-579-8	Sequence 8, Appl
420	21	42.9	8	4	US-10-367-658-247	Sequence 247, App	493	21	42.9	9	4	US-10-195-835-156	Sequence 156, App
421	21	42.9	8	4	US-10-367-668-247	Sequence 247, App	494	21	42.9	9	4	US-10-195-835-157	Sequence 157, App
422	21	42.9	8	4	US-10-367-674-247	Sequence 247, App	495	21	42.9	9	4	US-10-195-835-158	Sequence 158, App
423	21	42.9	8	4	US-10-712-425-634	Sequence 634, App	496	21	42.9	9	4	US-10-195-835-171	Sequence 171, App
424	21	42.9	8	4	US-10-712-425-725	Sequence 725, App	497	21	42.9	9	4	US-10-195-835-290	Sequence 290, App
425	21	42.9	8	4	US-10-712-425-726	Sequence 726, App	498	21	42.9	9	4	US-10-286-333-156	Sequence 156, App
426	21	42.9	8	4	US-10-712-425-727	Sequence 727, App	499	21	42.9	9	4	US-10-286-333-157	Sequence 157, App
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431	21	42.9	8	5	US-10-835-405-1	Sequence 1, Appl	504	21	42.9	9	4	US-10-244-830-157	Sequence 157, App
432	21	42.9	8	5	US-10-862-195-156	Sequence 156, App	505	21	42.9	9	4	US-10-244-830-158	Sequence 158, App
433	21	42.9	8	5	US-10-820-067A-226	Sequence 226, App	506	21	42.9	9	4	US-10-244-830-171	Sequence 171, App
434	21	42.9	8	5	US-09-775-805-56	Sequence 56, Appl	507	21	42.9	9	4	US-10-427-717-156	Sequence 156, App
435	21	42.9	9	3	US-09-915-543-8	Sequence 8, Appl	508	21	42.9	9	4	US-10-427-717-157	Sequence 157, App
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438	21	42.9	9	3	US-09-938-864-158	Sequence 158, App	511	21	42.9	9	4	US-10-427-717-290	Sequence 290, App
439	21	42.9	9	3	US-09-938-864-171	Sequence 171, App	512	21	42.9	9	4	US-10-664-859-8	Sequence 8, Appl
440	21	42.9	9	3	US-09-938-864-290	Sequence 290, App	513	21	42.9	9	4	US-10-398-104-54	Sequence 54, Appl
441	21	42.9	9	3	US-09-791-477-156	Sequence 156, App	514	21	42.9	9	4	US-10-182-252A-227	Sequence 227, App
442	21	42.9	9	3	US-09-791-477-157	Sequence 157, App	515	21	42.9	9	4	US-10-182-252A-295	Sequence 295, App
443	21	42.9	9	3	US-09-791-477-158	Sequence 158, App	516	21	42.9	9	4	US-10-182-252A-296	Sequence 296, App
444	21	42.9	9	3	US-09-791-477-171	Sequence 171, App	517	21	42.9	9	4	US-10-182-252A-297	Sequence 297, App
445	21	42.9	9	3	US-09-791-477-290	Sequence 290, App	518	21	42.9	9	4	US-10-182-252A-298	Sequence 298, App
446	21	42.9	9	3	US-09-785-019-156	Sequence 156, App	519	21	42.9	9	4	US-10-182-252A-364	Sequence 364, App
447	21	42.9	9	3	US-09-785-019-157	Sequence 157, App	520	21	42.9	9	4	US-10-182-252A-365	Sequence 365, App
448	21	42.9	9	3	US-09-785-019-158	Sequence 158, App	521	21	42.9	9	4	US-10-182-252A-397	Sequence 397, App
449	21	42.9	9	3	US-09-785-019-171	Sequence 171, App	522	21	42.9	9	4	US-10-182-252A-398	Sequence 398, App
450	21	42.9	9	3	US-09-785-019-290	Sequence 290, App	523	21	42.9	9	4	US-10-182-252A-400	Sequence 400, App
451	21	42.9	9	4	US-10-125-635A-156	Sequence 156, App	524	21	42.9	9	4	US-10-182-252A-399	Sequence 399, App
452	21	42.9	9	4	US-10-125-635A-157	Sequence 157, App	525	21	42.9	9	4	US-10-182-252A-443	Sequence 443, App
453	21	42.9	9	4	US-10-125-635A-158	Sequence 158, App	526	21	42.9	9	4	US-10-182-252A-444	Sequence 444, App
454	21	42.9	9	4	US-10-125-635A-171	Sequence 171, App	527	21	42.9	9	4	US-10-182-252A-401	Sequence 401, App
455	21	42.9	9	4	US-10-125-635A-290	Sequence 290, App	528	21	42.9	9	4	US-10-182-252A-402	Sequence 402, App
456	21	42.9	9	4	US-10-001-469-45	Sequence 45, Appl	529	21	42.9	9	4	US-10-182-252A-441	Sequence 441, App
457	21	42.9	9	4	US-10-001-469-56	Sequence 56, Appl	530	21	42.9	9	4	US-10-182-252A-442	Sequence 442, App
458	21	42.9	9	4	US-10-001-469-91	Sequence 91, Appl	531	21	42.9	9	4	US-10-182-252A-443	Sequence 443, App
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460	21	42.9	9	4	US-10-001-469-259	Sequence 259, App	533	21	42.9	9	4	US-10-182-252A-446	Sequence 446, App
461	21	42.9	9	4	US-10-001-469-286	Sequence 286, App	534	21	42.9	9	4	US-10-182-252A-447	Sequence 447, App
462	21	42.9	9	4	US-10-001-469-447	Sequence 447, App	535	21	42.9	9	4	US-10-182-252A-448	Sequence 448, App
463	21	42.9	9	4	US-10-001-469-465	Sequence 465, App	536	21	42.9	9	4	US-10-182-252A-841	Sequence 841, App
464	21	42.9	9	4	US-10-001-469-493	Sequence 493, App	537	21	42.9	9	4	US-10-182-252A-1114	Sequence 1114, App
465	21	42.9	9	4	US-10-001-469-644	Sequence 644, App	538	21	42.9	9	4	US-10-182-252A-1115	Sequence 1115, App

539	21	42.9	9	4	US-10-182-252A-1116	Sequence 1116, Ap	612	20	40.8	7	5	US-10-509-307-85	Sequence 85, Appl
540	21	42.9	9	4	US-10-182-252A-1117	Sequence 1117, Ap	613	20	40.8	7	5	US-10-691-532-3	Sequence 3, Appl
541	21	42.9	9	4	US-10-182-252A-1118	Sequence 1118, Ap	614	20	40.8	7	5	US-10-862-195-1579	Sequence 1579, Ap
542	21	42.9	9	4	US-10-182-252A-1119	Sequence 1119, Ap	615	20	40.8	7	5	US-10-618-779-62	Sequence 62, Appl
543	21	42.9	9	4	US-10-182-252A-1120	Sequence 1120, Ap	616	20	40.8	7	5	US-09-833-203-39	Sequence 39, Appl
544	21	42.9	9	4	US-10-182-252A-1121	Sequence 1121, Ap	617	20	40.8	8	3	US-10-094-699-26	Sequence 26, Appl
545	21	42.9	9	4	US-10-182-252A-1122	Sequence 1122, Ap	618	20	40.8	8	4	US-10-226-007-491	Sequence 491, Appl
546	21	42.9	9	4	US-10-182-252A-1123	Sequence 1123, Ap	619	20	40.8	8	4	US-10-224-999A-2605	Sequence 2605, Ap
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548	21	42.9	9	4	US-10-182-252A-1125	Sequence 1125, Ap	621	20	40.8	8	4	US-10-224-999A-2607	Sequence 2607, Ap
549	21	42.9	9	4	US-10-182-252A-1126	Sequence 1126, Ap	622	20	40.8	8	4	US-10-224-999A-2748	Sequence 2748, Ap
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551	21	42.9	9	4	US-10-182-252A-1128	Sequence 1128, Ap	624	20	40.8	8	4	US-10-224-999A-2750	Sequence 2750, Ap
552	21	42.9	9	4	US-10-182-252A-1129	Sequence 1129, Ap	625	20	40.8	8	4	US-10-357-939A-43	Sequence 43, Appl
553	21	42.9	9	4	US-10-182-252A-1130	Sequence 1130, Ap	626	20	40.8	8	4	US-10-117-937-53	Sequence 53, Appl
554	21	42.9	9	4	US-10-182-252A-1131	Sequence 1131, Ap	627	20	40.8	8	4	US-10-121-456A-4	Sequence 4, Appl
555	21	42.9	9	4	US-10-182-252A-1263	Sequence 1263, Ap	628	20	40.8	8	4	US-10-657-022-53	Sequence 53, Appl
556	21	42.9	9	4	US-10-182-252A-1264	Sequence 1264, Ap	629	20	40.8	8	4	US-10-809-790-8	Sequence 8, Appl
557	21	42.9	9	4	US-10-182-252A-1265	Sequence 1265, Ap	630	20	40.8	8	4	US-10-950-163-138	Sequence 138, Appl
558	21	42.9	9	4	US-10-182-252A-1266	Sequence 1266, Ap	631	20	40.8	8	5	US-10-950-163-139	Sequence 139, Appl
559	21	42.9	9	4	US-10-648-780-156	Sequence 156, Ap	632	20	40.8	8	5	US-10-950-163-140	Sequence 140, Appl
560	21	42.9	9	4	US-10-648-780-157	Sequence 157, Ap	633	20	40.8	8	5	US-10-950-163-141	Sequence 141, Appl
561	21	42.9	9	4	US-10-648-780-158	Sequence 158, Ap	634	20	40.8	8	5	US-10-862-195-144	Sequence 144, Appl
562	21	42.9	9	4	US-10-648-780-171	Sequence 171, Ap	635	20	40.8	8	6	US-11-067-084-53	Sequence 53, Appl
563	21	42.9	9	4	US-10-648-780-230	Sequence 230, Ap	636	20	40.8	8	6	US-11-051-411-405	Sequence 405, Appl
564	21	42.9	9	4	US-10-364-645A-19	Sequence 19, Appl	637	20	40.8	8	6	US-11-051-411-590	Sequence 590, Appl
565	21	42.9	9	4	US-10-753-339-56	Sequence 56, Appl	638	20	40.8	8	6	US-11-067-159-53	Sequence 53, Appl
566	21	42.9	9	4	US-10-611-440-94	Sequence 94, Appl	639	20	40.8	9	3	US-09-829-549A-22	Sequence 22, Appl
567	21	42.9	9	4	US-10-611-440-187	Sequence 187, Ap	640	20	40.8	9	3	US-09-935-430-7	Sequence 7, Appl
568	21	42.9	9	4	US-10-611-440-188	Sequence 188, Ap	641	20	40.8	9	3	US-09-898-860-14	Sequence 14, Appl
569	21	42.9	9	5	US-10-862-195-291	Sequence 291, Ap	642	20	40.8	9	3	US-09-854-248-29	Sequence 29, Appl
570	21	42.9	9	5	US-10-862-195-295	Sequence 295, Ap	643	20	40.8	9	4	US-10-094-699-20	Sequence 20, Appl
571	21	42.9	9	5	US-10-862-195-1297	Sequence 1297, Ap	644	20	40.8	9	4	US-10-094-699-24	Sequence 24, Appl
572	20	40.8	5	4	US-10-074-225A-10	Sequence 10, Appl	645	20	40.8	9	4	US-10-094-699-44	Sequence 44, Appl
573	20	40.8	5	4	US-10-096-986-3	Sequence 3, Appl	646	20	40.8	9	4	US-10-014-340-635	Sequence 635, Appl
574	20	40.8	5	4	US-10-437-708-4	Sequence 4, Appl	647	20	40.8	9	4	US-10-211-088-349	Sequence 349, Appl
575	20	40.8	5	4	US-10-395-402-4	Sequence 4, Appl	648	20	40.8	9	4	US-10-226-007-492	Sequence 492, Appl
576	20	40.8	5	5	US-10-257-199-4	Sequence 4, Appl	649	20	40.8	9	4	US-10-226-007-504	Sequence 504, Appl
577	20	40.8	5	5	US-10-808-187-598	Sequence 598, Ap	650	20	40.8	9	4	US-10-219-850-3	Sequence 3, Appl
578	20	40.8	5	5	US-10-418-032-4	Sequence 4, Appl	651	20	40.8	9	4	US-10-197-954-116	Sequence 116, Appl
579	20	40.8	5	5	US-10-418-032-239	Sequence 239, Ap	652	20	40.8	9	4	US-10-224-999A-2610	Sequence 2610, Appl
580	20	40.8	5	5	US-10-507-734-30	Sequence 30, Appl	653	20	40.8	9	4	US-10-224-999A-2611	Sequence 2611, Appl
581	20	40.8	5	5	US-10-807-807-598	Sequence 598, Ap	654	20	40.8	9	4	US-10-224-999A-2612	Sequence 2612, Appl
582	20	40.8	6	3	US-09-766-167-24	Sequence 24, Appl	655	20	40.8	9	4	US-10-224-999A-2613	Sequence 2613, Appl
583	20	40.8	6	4	US-10-208-557-24	Sequence 24, Appl	656	20	40.8	9	4	US-10-224-999A-2753	Sequence 2753, Appl
584	20	40.8	6	4	US-10-307-956-16	Sequence 16, Appl	657	20	40.8	9	4	US-10-224-999A-2754	Sequence 2754, Appl
585	20	40.8	6	4	US-10-315-964A-403	Sequence 403, Ap	658	20	40.8	9	4	US-10-224-999A-2755	Sequence 2755, Appl
586	20	40.8	6	4	US-10-317-251A-403	Sequence 403, Ap	659	20	40.8	9	4	US-10-277-292-7	Sequence 7, Appl
587	20	40.8	6	4	US-10-184-771-14	Sequence 14, Appl	660	20	40.8	9	4	US-10-280-340-7	Sequence 7, Appl
588	20	40.8	6	4	US-10-414-524-97	Sequence 97, Appl	661	20	40.8	9	4	US-10-334-726-98	Sequence 98, Appl
589	20	40.8	6	4	US-10-774-938-24	Sequence 24, Appl	662	20	40.8	9	4	US-10-117-937-47	Sequence 47, Appl
590	20	40.8	6	5	US-10-986-646-24	Sequence 24, Appl	663	20	40.8	9	4	US-10-117-937-51	Sequence 51, Appl
591	20	40.8	6	5	US-11-064-196-14	Sequence 14, Appl	664	20	40.8	9	4	US-10-117-937-243	Sequence 243, Appl
592	20	40.8	6	6	US-09-731-242A-22	Sequence 22, Appl	665	20	40.8	9	4	US-10-245-871-534	Sequence 534, Appl
593	20	40.8	7	3	US-09-954-385-203	Sequence 203, Ap	666	20	40.8	9	4	US-10-353-678-9	Sequence 9, Appl
594	20	40.8	7	3	US-09-954-385-242	Sequence 242, Ap	667	20	40.8	9	4	US-10-121-456A-5	Sequence 5, Appl
595	20	40.8	7	3	US-09-800-187-18	Sequence 18, Appl	668	20	40.8	9	4	US-10-671-403-9	Sequence 9, Appl
596	20	40.8	7	3	US-09-800-187-49	Sequence 49, Appl	669	20	40.8	9	4	US-10-671-419-9	Sequence 9, Appl
597	20	40.8	7	3	US-09-800-187-50	Sequence 50, Appl	670	20	40.8	9	4	US-10-670-844-9	Sequence 9, Appl
598	20	40.8	7	3	US-09-800-187-51	Sequence 51, Appl	671	20	40.8	9	4	US-10-671-134-9	Sequence 9, Appl
599	20	40.8	7	3	US-09-800-187-52	Sequence 52, Appl	672	20	40.8	9	4	US-10-363-208-125	Sequence 125, Appl
600	20	40.8	7	3	US-09-800-187-53	Sequence 53, Appl	673	20	40.8	9	4	US-10-673-098-9	Sequence 9, Appl
601	20	40.8	7	3	US-09-957-806A-242	Sequence 242, Ap	674	20	40.8	9	4	US-10-253-286-534	Sequence 534, Appl
602	20	40.8	7	4	US-10-163-415-8	Sequence 3, Appl	675	20	40.8	9	4	US-10-182-252A-75	Sequence 75, Appl
603	20	40.8	7	4	US-10-121-456A-3	Sequence 308, Appl	676	20	40.8	9	4	US-10-182-252A-76	Sequence 76, Appl
604	20	40.8	7	4	US-10-398-104-308	Sequence 310, Ap	677	20	40.8	9	4	US-10-182-252A-795	Sequence 795, Appl
605	20	40.8	7	4	US-10-398-104-310	Sequence 22, Appl	678	20	40.8	9	4	US-10-617-876-51	Sequence 51, Appl
606	20	40.8	7	4	US-10-783-786-22	Sequence 203, Ap	679	20	40.8	9	4	US-10-672-638-9	Sequence 9, Appl
607	20	40.8	7	5	US-10-912-512-203	Sequence 242, Ap	680	20	40.8	9	4	US-10-673-127-9	Sequence 9, Appl
608	20	40.8	7	5	US-10-912-512-242	Sequence 203, Ap	681	20	40.8	9	4	US-10-670-817-9	Sequence 9, Appl
609	20	40.8	7	5	US-10-235-043-203	Sequence 242, Ap	682	20	40.8	9	4	US-10-657-022-47	Sequence 47, Appl
610	20	40.8	7	5	US-10-235-043-242	Sequence 242, Ap	683	20	40.8	9	4	US-10-657-022-51	Sequence 51, Appl
611	20	40.8	7	5			684	20	40.8	9	4		

685	20	40.8	9	4	US-10-671-207-9	Sequence 9, Appli	758	19	38.8	7	4	US-10-352-786-266	Sequence 266, App
686	20	40.8	9	4	US-10-685-977-14	Sequence 14, Appl	759	19	38.8	7	4	US-10-352-786-268	Sequence 268, App
687	20	40.8	9	5	US-10-760-085-116	Sequence 116, Appl	760	19	38.8	7	4	US-10-352-786-270	Sequence 270, App
688	20	40.8	9	5	US-10-673-120-9	Sequence 9, Appli	761	19	38.8	7	4	US-10-460-594-23	Sequence 23, Appl
689	20	40.8	9	5	US-10-838-289-306	Sequence 306, App	762	19	38.8	7	4	US-10-258-146A-46	Sequence 46, Appl
690	20	40.8	9	5	US-10-607-595-249	Sequence 249, App	763	19	38.8	7	4	US-10-258-146A-122	Sequence 122, App
691	20	40.8	9	5	US-10-671-412-9	Sequence 9, Appli	764	19	38.8	7	4	US-10-258-146A-156	Sequence 156, App
692	20	40.8	9	5	US-10-671-859-9	Sequence 9, Appli	765	19	38.8	7	4	US-10-423-543-52	Sequence 52, Appl
693	20	40.8	9	5	US-10-671-106-9	Sequence 9, Appli	766	19	38.8	7	4	US-10-328-953-191	Sequence 191, App
694	20	40.8	9	5	US-10-948-707-425	Sequence 425, App	767	19	38.8	7	4	US-10-328-953-267	Sequence 267, App
695	20	40.8	9	5	US-10-990-137-7	Sequence 7, Appli	768	19	38.8	7	4	US-10-328-953-301	Sequence 301, App
696	20	40.8	9	6	US-11-067-064-47	Sequence 47, Appl	769	19	38.8	7	4	US-10-610-927-7	Sequence 7, Appli
697	20	40.8	9	6	US-11-067-064-51	Sequence 51, Appl	770	19	38.8	7	4	US-10-610-927-10	Sequence 10, Appl
698	20	40.8	9	6	US-11-067-064-243	Sequence 243, App	771	19	38.8	7	4	US-10-610-927-12	Sequence 12, Appl
699	20	40.8	9	6	US-11-066-697-1346	Sequence 1346, Ap	772	19	38.8	7	4	US-10-610-927-13	Sequence 13, Appl
700	20	40.8	9	6	US-11-067-159-47	Sequence 47, Appl	773	19	38.8	7	4	US-10-610-927-14	Sequence 14, Appl
701	20	40.8	9	6	US-11-067-159-51	Sequence 51, Appl	774	19	38.8	7	4	US-10-610-927-15	Sequence 15, Appl
702	20	40.8	9	6	US-11-067-159-243	Sequence 243, App	775	19	38.8	7	4	US-10-610-927-16	Sequence 16, Appl
703	19, 5	39.8	9	4	US-10-149-137A-465	Sequence 465, App	776	19	38.8	7	4	US-10-258-144-81	Sequence 81, Appl
704	19	38.8	5	3	US-09-972-035A-10	Sequence 10, Appl	777	19	38.8	7	4	US-10-258-144-157	Sequence 157, App
705	19	38.8	5	4	US-10-093-895-25	Sequence 25, Appl	778	19	38.8	7	4	US-10-258-144-191	Sequence 191, App
706	19	38.8	5	4	US-10-185-050-233	Sequence 233, App	779	19	38.8	7	4	US-10-663-407-18	Sequence 18, Appl
707	19	38.8	5	4	US-10-223-172A-10	Sequence 10, Appl	780	19	38.8	7	5	US-10-613-380-20	Sequence 20, Appl
708	19	38.8	5	4	US-10-224-999A-10	Sequence 10, Appl	781	19	38.8	7	5	US-10-912-512-39	Sequence 39, Appl
709	19	38.8	5	4	US-10-352-786-129	Sequence 129, App	782	19	38.8	7	5	US-10-912-512-86	Sequence 86, Appl
710	19	38.8	5	4	US-10-663-407-10	Sequence 10, Appl	783	19	38.8	7	5	US-10-912-512-208	Sequence 208, App
711	19	38.8	5	4	US-10-703-195-30	Sequence 30, Appl	784	19	38.8	7	5	US-10-235-043-39	Sequence 39, Appl
712	19	38.8	5	5	US-10-653-706-8	Sequence 8, Appli	785	19	38.8	7	5	US-10-235-043-86	Sequence 86, Appl
713	19	38.8	5	5	US-10-653-706-9	Sequence 9, Appli	786	19	38.8	7	5	US-10-235-043-208	Sequence 208, App
714	19	38.8	6	3	US-09-873-106B-10	Sequence 10, Appl	787	19	38.8	7	5	US-10-862-195-1512	Sequence 1512, Ap
715	19	38.8	6	3	US-09-972-035A-12	Sequence 12, Appl	788	19	38.8	7	5	US-10-820-067A-501	Sequence 501, App
716	19	38.8	6	3	US-09-943-944E-75	Sequence 75, Appl	789	19	38.8	7	5	US-10-820-067A-577	Sequence 577, App
717	19	38.8	6	4	US-10-223-172A-12	Sequence 12, Appl	790	19	38.8	7	5	US-10-820-067A-611	Sequence 611, App
718	19	38.8	6	4	US-10-315-964A-392	Sequence 392, App	791	19	38.8	8	3	US-09-879-936-19	Sequence 19, Appl
719	19	38.8	6	4	US-10-315-964A-393	Sequence 393, App	792	19	38.8	8	3	US-09-972-035A-20	Sequence 20, Appl
720	19	38.8	6	4	US-10-317-251A-392	Sequence 392, App	793	19	38.8	8	4	US-10-136-734-17	Sequence 17, Appl
721	19	38.8	6	4	US-10-317-251A-393	Sequence 393, App	794	19	38.8	8	4	US-10-235-552-6	Sequence 6, Appli
722	19	38.8	6	4	US-10-317-252A-392	Sequence 392, App	795	19	38.8	8	4	US-10-283-838-21	Sequence 21, Appl
723	19	38.8	6	4	US-10-317-252A-393	Sequence 393, App	796	19	38.8	8	4	US-10-286-007-26	Sequence 26, Appl
724	19	38.8	6	4	US-10-184-771-15	Sequence 15, Appl	797	19	38.8	8	4	US-10-226-007-478	Sequence 478, App
725	19	38.8	6	4	US-10-224-999A-12	Sequence 12, Appl	798	19	38.8	8	4	US-10-052-578-23	Sequence 23, Appl
726	19	38.8	6	4	US-10-352-786-195	Sequence 195, App	799	19	38.8	8	4	US-10-052-578-94	Sequence 94, Appl
727	19	38.8	6	4	US-10-352-786-197	Sequence 197, App	800	19	38.8	8	4	US-10-223-172A-20	Sequence 20, Appl
728	19	38.8	6	4	US-10-663-407-12	Sequence 12, Appl	801	19	38.8	8	4	US-10-283-423-165	Sequence 165, App
729	19	38.8	6	5	US-10-912-764-21	Sequence 21, Appl	802	19	38.8	8	4	US-10-053-520-23	Sequence 23, Appl
730	19	38.8	6	6	US-11-064-196-15	Sequence 15, Appl	803	19	38.8	8	4	US-10-053-520-94	Sequence 94, Appl
731	19	38.8	6	6	US-11-066-697-1217	Sequence 1217, Ap	804	19	38.8	8	4	US-10-175-270-10	Sequence 10, Appl
732	19	38.8	7	2	US-08-769-250A-7	Sequence 7, Appli	805	19	38.8	8	4	US-10-224-999A-20	Sequence 20, Appl
733	19	38.8	7	2	US-08-769-250A-10	Sequence 10, Appl	806	19	38.8	8	4	US-10-224-999A-2604	Sequence 2604, Ap
734	19	38.8	7	2	US-08-769-250A-12	Sequence 12, Appl	807	19	38.8	8	4	US-10-224-999A-2747	Sequence 2747, Ap
735	19	38.8	7	2	US-08-769-250A-13	Sequence 13, Appl	808	19	38.8	8	4	US-10-008-524A-22	Sequence 22, Appl
736	19	38.8	7	2	US-08-769-250A-14	Sequence 14, Appl	809	19	38.8	8	4	US-10-008-524A-23	Sequence 23, Appl
737	19	38.8	7	2	US-08-769-250A-15	Sequence 15, Appl	810	19	38.8	8	4	US-10-008-524A-24	Sequence 24, Appl
738	19	38.8	7	2	US-08-769-250A-16	Sequence 16, Appl	811	19	38.8	8	4	US-10-008-524A-25	Sequence 25, Appl
739	19	38.8	7	3	US-09-794-960-6	Sequence 6, Appli	812	19	38.8	8	4	US-10-008-524A-26	Sequence 26, Appl
740	19	38.8	7	3	US-09-947-137-12	Sequence 12, Appl	813	19	38.8	8	4	US-10-213-821-165	Sequence 165, App
741	19	38.8	7	3	US-09-947-137-27	Sequence 27, Appl	814	19	38.8	8	4	US-10-053-498B-23	Sequence 23, Appl
742	19	38.8	7	3	US-09-972-035A-18	Sequence 18, Appl	815	19	38.8	8	4	US-10-053-498B-94	Sequence 94, Appli
743	19	38.8	7	3	US-09-954-385-39	Sequence 39, Appl	816	19	38.8	8	4	US-10-181-546-1	Sequence 1, Appli
744	19	38.8	7	3	US-09-954-385-86	Sequence 86, Appl	817	19	38.8	8	4	US-10-350-719-22	Sequence 22, Appl
745	19	38.8	7	3	US-09-954-385-208	Sequence 208, App	818	19	38.8	8	4	US-10-350-719-23	Sequence 23, Appl
746	19	38.8	7	4	US-10-052-578-188	Sequence 188, App	819	19	38.8	8	4	US-10-350-719-24	Sequence 24, Appl
747	19	38.8	7	4	US-10-052-578-264	Sequence 264, App	820	19	38.8	8	4	US-10-350-719-25	Sequence 25, Appl
748	19	38.8	7	4	US-10-052-578-298	Sequence 298, App	821	19	38.8	8	4	US-10-350-719-26	Sequence 26, Appl
749	19	38.8	7	4	US-10-223-172A-18	Sequence 18, Appl	822	19	38.8	8	4	US-10-352-786-339	Sequence 339, App
750	19	38.8	7	4	US-10-286-457-220	Sequence 220, App	823	19	38.8	8	4	US-10-352-786-341	Sequence 341, App
751	19	38.8	7	4	US-10-053-520-188	Sequence 188, App	824	19	38.8	8	4	US-10-352-786-343	Sequence 343, App
752	19	38.8	7	4	US-10-053-520-264	Sequence 264, App	825	19	38.8	8	4	US-10-352-786-345	Sequence 345, App
753	19	38.8	7	4	US-10-053-520-298	Sequence 298, App	826	19	38.8	8	4	US-10-442-909-64	Sequence 64, Appl
754	19	38.8	7	4	US-10-224-999A-18	Sequence 18, Appl	827	19	38.8	8	4	US-10-442-909-65	Sequence 65, Appl
755	19	38.8	7	4	US-10-053-498B-188	Sequence 188, App	828	19	38.8	8	4	US-10-328-953-104	Sequence 104, App
756	19	38.8	7	4	US-10-053-498B-264	Sequence 264, App	829	19	38.8	8	4	US-10-328-953-138	Sequence 138, App
757	19	38.8	7	4	US-10-053-498B-298	Sequence 298, App	830	19	38.8	8	4	US-10-663-407-20	Sequence 20, Appl

831	19	38.8	8	4	US-10-736-048-165	Sequence 165, App	904	19	38.8	9	4	US-10-280-340-11	Sequence 11, Appl
832	19	38.8	8	4	US-10-712-425-1138	Sequence 1138, App	905	19	38.8	9	4	US-10-280-340-467	Sequence 467, App
833	19	38.8	8	5	US-10-654-601-8	Sequence 8, Appl	906	19	38.8	9	4	US-10-280-340-552	Sequence 552, App
834	19	38.8	8	5	US-10-654-601-201	Sequence 201, App	907	19	38.8	9	4	US-10-334-726-35	Sequence 35, Appl
835	19	38.8	8	5	US-10-654-601-1326	Sequence 1326, App	908	19	38.8	9	4	US-10-334-726-187	Sequence 187, App
836	19	38.8	8	5	US-10-773-032-1138	Sequence 1138, App	909	19	38.8	9	4	US-10-334-726-223	Sequence 223, App
837	19	38.8	8	5	US-10-833-405-2	Sequence 2, Appl	910	19	38.8	9	4	US-10-371-069-370	Sequence 370, App
838	19	38.8	8	5	US-10-862-195-157	Sequence 157, App	911	19	38.8	9	4	US-10-371-069-404	Sequence 404, App
839	19	38.8	8	5	US-10-862-195-1511	Sequence 1511, App	912	19	38.8	9	4	US-10-371-645-370	Sequence 370, App
840	19	38.8	8	5	US-10-776-521B-232	Sequence 232, App	913	19	38.8	9	4	US-10-371-645-404	Sequence 404, App
841	19	38.8	8	5	US-10-776-521B-308	Sequence 308, App	914	19	38.8	9	4	US-10-117-937-249	Sequence 249, App
842	19	38.8	8	5	US-10-776-521B-342	Sequence 342, App	915	19	38.8	9	4	US-10-371-260-370	Sequence 370, App
843	19	38.8	8	5	US-10-820-067A-414	Sequence 414, App	916	19	38.8	9	4	US-10-371-260-404	Sequence 404, App
844	19	38.8	8	5	US-10-820-067A-448	Sequence 448, App	917	19	38.8	9	4	US-10-352-786-415	Sequence 415, App
845	19	38.8	8	5	US-10-820-067A-742	Sequence 742, App	918	19	38.8	9	4	US-10-352-786-417	Sequence 417, App
846	19	38.8	8	5	US-10-820-067A-818	Sequence 818, App	919	19	38.8	9	4	US-10-352-786-419	Sequence 419, App
847	19	38.8	8	5	US-10-820-067A-852	Sequence 852, App	920	19	38.8	9	4	US-10-352-786-421	Sequence 421, App
848	19	38.8	8	5	US-10-806-062-131	Sequence 131, App	921	19	38.8	9	4	US-10-352-786-424	Sequence 424, App
849	19	38.8	9	2	US-08-801-405B-4	Sequence 4, Appl	922	19	38.8	9	4	US-10-352-786-425	Sequence 425, App
850	19	38.8	9	2	US-08-854-825-43	Sequence 43, Appl	923	19	38.8	9	4	US-10-410-894-21	Sequence 21, Appl
851	19	38.8	9	3	US-09-065-902-17	Sequence 17, Appl	924	19	38.8	9	4	US-10-245-871-288	Sequence 288, App
852	19	38.8	9	3	US-09-861-294-37	Sequence 37, Appl	925	19	38.8	9	4	US-10-442-909-18	Sequence 18, Appl
853	19	38.8	9	3	US-09-894-018-170	Sequence 170, App	926	19	38.8	9	4	US-10-057-475B-10870	Sequence 10870, A
854	19	38.8	9	3	US-09-894-018-332	Sequence 332, App	927	19	38.8	9	4	US-10-057-475B-10923	Sequence 10923, A
855	19	38.8	9	3	US-09-753-831-7	Sequence 7, Appl	928	19	38.8	9	4	US-10-057-475B-10929	Sequence 10929, A
856	19	38.8	9	3	US-09-972-035A-24	Sequence 24, Appl	929	19	38.8	9	4	US-10-154-884B-10870	Sequence 10870, A
857	19	38.8	9	3	US-09-017-743C-11	Sequence 11, Appl	930	19	38.8	9	4	US-10-154-884B-10923	Sequence 10923, A
858	19	38.8	9	3	US-09-017-743C-76	Sequence 76, Appl	931	19	38.8	9	4	US-10-154-884B-10923	Sequence 10929, A
859	19	38.8	9	3	US-09-017-743C-77	Sequence 77, Appl	932	19	38.8	9	4	US-10-121-456A-7	Sequence 7, Appl
860	19	38.8	9	3	US-09-367-703-5	Sequence 5, Appl	933	19	38.8	9	4	US-10-114-669-143	Sequence 143, App
861	19	38.8	9	3	US-09-935-430-11	Sequence 11, Appl	934	19	38.8	9	4	US-10-114-669-146	Sequence 146, App
862	19	38.8	9	3	US-09-935-430-467	Sequence 467, App	935	19	38.8	9	4	US-10-114-669-163	Sequence 163, App
863	19	38.8	9	3	US-09-935-430-552	Sequence 552, App	936	19	38.8	9	4	US-10-114-669-168	Sequence 168, App
864	19	38.8	9	3	US-09-983-802-312	Sequence 312, App	937	19	38.8	9	4	US-10-114-669-485	Sequence 485, App
865	19	38.8	9	3	US-09-821-734-4	Sequence 4, Appl	938	19	38.8	9	4	US-10-114-669-504	Sequence 504, App
866	19	38.8	9	3	US-09-788-308D-1	Sequence 1, Appl	939	19	38.8	9	4	US-10-114-669-507	Sequence 507, App
867	19	38.8	9	3	US-09-984-490-312	Sequence 312, App	940	19	38.8	9	4	US-10-114-669-508	Sequence 508, App
868	19	38.8	9	3	US-09-978-309A-39	Sequence 39, Appl	941	19	38.8	9	4	US-10-114-669-831	Sequence 831, App
869	19	38.8	9	3	US-09-978-309A-43	Sequence 43, Appl	942	19	38.8	9	4	US-10-114-669-841	Sequence 841, App
870	19	38.8	9	3	US-09-854-248-11	Sequence 11, Appl	943	19	38.8	9	4	US-10-114-669-843	Sequence 843, App
871	19	38.8	9	3	US-09-833-039-20	Sequence 20, Appl	944	19	38.8	9	4	US-10-114-669-850	Sequence 850, App
872	19	38.8	9	3	US-09-278-278-287	Sequence 287, App	945	19	38.8	9	4	US-10-114-669-1149	Sequence 1149, App
873	19	38.8	9	4	US-10-094-699-50	Sequence 50, Appl	946	19	38.8	9	4	US-10-114-669-1157	Sequence 1157, App
874	19	38.8	9	4	US-10-062-710-59	Sequence 59, Appl	947	19	38.8	9	4	US-10-114-669-1176	Sequence 1176, App
875	19	38.8	9	4	US-10-226-007-479	Sequence 479, App	948	19	38.8	9	4	US-10-114-669-1182	Sequence 1182, App
876	19	38.8	9	4	US-10-254-446A-109	Sequence 109, App	949	19	38.8	9	4	US-10-114-669-1511	Sequence 1511, App
877	19	38.8	9	4	US-10-223-172A-24	Sequence 24, Appl	950	19	38.8	9	4	US-10-114-669-1538	Sequence 1538, App
878	19	38.8	9	4	US-10-223-172A-27	Sequence 27, Appl	951	19	38.8	9	4	US-10-114-669-1543	Sequence 1543, App
879	19	38.8	9	4	US-10-116-118-47	Sequence 47, Appl	952	19	38.8	9	4	US-10-114-669-1550	Sequence 1550, App
880	19	38.8	9	4	US-10-062-109A-33	Sequence 33, Appl	953	19	38.8	9	4	US-10-114-669-1845	Sequence 1845, App
881	19	38.8	9	4	US-10-062-109A-37	Sequence 37, Appl	954	19	38.8	9	4	US-10-114-669-1868	Sequence 1868, App
882	19	38.8	9	4	US-10-062-109A-287	Sequence 287, App	955	19	38.8	9	4	US-10-114-669-1876	Sequence 1876, App
883	19	38.8	9	4	US-10-062-109A-368	Sequence 368, App	956	19	38.8	9	4	US-10-114-669-1877	Sequence 1877, App
884	19	38.8	9	4	US-10-062-109A-654	Sequence 654, App	957	19	38.8	9	4	US-10-114-669-2183	Sequence 2183, App
885	19	38.8	9	4	US-10-022-066-341	Sequence 341, App	958	19	38.8	9	4	US-10-114-669-2222	Sequence 2222, App
886	19	38.8	9	4	US-10-022-066-384	Sequence 384, App	959	19	38.8	9	4	US-10-114-669-2223	Sequence 2223, App
887	19	38.8	9	4	US-10-224-999A-24	Sequence 24, Appl	960	19	38.8	9	4	US-10-114-669-2230	Sequence 2230, App
888	19	38.8	9	4	US-10-224-999A-27	Sequence 27, Appl	961	19	38.8	9	4	US-10-114-669-5006	Sequence 5006, App
889	19	38.8	9	4	US-10-224-999A-2609	Sequence 2609, App	962	19	38.8	9	4	US-10-114-669-5027	Sequence 5027, App
890	19	38.8	9	4	US-10-224-999A-2752	Sequence 2752, App	963	19	38.8	9	4	US-10-114-669-5029	Sequence 5029, App
891	19	38.8	9	4	US-10-364-614-3	Sequence 3, Appl	964	19	38.8	9	4	US-10-114-669-5038	Sequence 5038, App
892	19	38.8	9	4	US-10-239-313A-269	Sequence 269, App	965	19	38.8	9	4	US-10-114-669-5054	Sequence 5054, App
893	19	38.8	9	4	US-10-239-313A-271	Sequence 271, App	966	19	38.8	9	4	US-10-114-669-5060	Sequence 5060, App
894	19	38.8	9	4	US-10-177-277-20	Sequence 20, Appl	967	19	38.8	9	4	US-10-114-669-5067	Sequence 5067, App
895	19	38.8	9	4	US-10-005-480A-33	Sequence 33, Appl	968	19	38.8	9	4	US-10-114-669-5110	Sequence 5110, App
896	19	38.8	9	4	US-10-005-480A-287	Sequence 287, App	969	19	38.8	9	4	US-10-114-669-5122	Sequence 5122, App
897	19	38.8	9	4	US-10-005-480A-368	Sequence 368, App	970	19	38.8	9	4	US-10-114-669-5128	Sequence 5128, App
898	19	38.8	9	4	US-10-005-480A-654	Sequence 654, App	971	19	38.8	9	4	US-10-114-669-5133	Sequence 5133, App
899	19	38.8	9	4	US-10-277-292-11	Sequence 11, Appl	972	19	38.8	9	4	US-10-114-669-5177	Sequence 5177, App
900	19	38.8	9	4	US-10-277-292-467	Sequence 467, App	973	19	38.8	9	4	US-10-114-669-5182	Sequence 5182, App
901	19	38.8	9	4	US-10-277-292-552	Sequence 552, App	974	19	38.8	9	4	US-10-114-669-5204	Sequence 5204, App
902	19	38.8	9	4	US-10-371-525-975	Sequence 370, App	975	19	38.8	9	4	US-10-114-669-5255	Sequence 5255, App
903	19	38.8	9	4	US-10-371-525-404	Sequence 404, App	976	19	38.8	9	4	US-10-114-669-5261	Sequence 5261, App

977 19 38.8 9 4 US-10-114-669-5274 Sequence 5274, Ap
978 19 38.8 9 4 US-10-114-669-5275 Sequence 5275, Ap
979 19 38.8 9 4 US-10-114-669-5317 Sequence 5317, Ap
980 19 38.8 9 4 US-10-114-669-5327 Sequence 5327, Ap
981 19 38.8 9 4 US-10-114-669-5350 Sequence 5350, Ap
982 19 38.8 9 4 US-10-114-669-5354 Sequence 5354, Ap
983 19 38.8 9 4 US-10-114-669-5365 Sequence 5365, Ap
984 19 38.8 9 4 US-10-114-669-5385 Sequence 5385, Ap
985 19 38.8 9 4 US-10-114-669-5404 Sequence 5404, Ap
986 19 38.8 9 4 US-10-114-669-5418 Sequence 5418, Ap
987 19 38.8 9 4 US-10-114-669-5430 Sequence 5430, Ap
988 19 38.8 9 4 US-10-114-669-5431 Sequence 5431, Ap
989 19 38.8 9 4 US-10-114-669-5471 Sequence 5471, Ap
990 19 38.8 9 4 US-10-114-669-5493 Sequence 5493, Ap
991 19 38.8 9 4 US-10-114-669-5494 Sequence 5494, Ap
992 19 38.8 9 4 US-10-114-669-5495 Sequence 5495, Ap
993 19 38.8 9 4 US-10-114-669-5535 Sequence 5535, Ap
994 19 38.8 9 4 US-10-114-669-5548 Sequence 5548, Ap
995 19 38.8 9 4 US-10-114-669-5568 Sequence 5568, Ap
996 19 38.8 9 4 US-10-114-669-5569 Sequence 5569, Ap
997 19 38.8 9 4 US-10-114-669-5609 Sequence 5609, Ap
998 19 38.8 9 4 US-10-114-669-5616 Sequence 5616, Ap
999 19 38.8 9 4 US-10-365-761B-75 Sequence 75, Appl
1000 19 38.8 9 4 US-10-620-462-5 Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-10-447-161-98
; Sequence 98, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-98

Query Match 100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPPVHNV 9
| | | | | | | | | |
Db 1 STAPPVHNV 9

RESULT 2
US-09-909-460-55
; Sequence 55, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-460-55

Query Match 79.6%; Score 39; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STAPPVHNV 9
| | | | | | | | | |
Db 1 STAPPVHNV 9

RESULT 3
US-09-872-836-55
; Sequence 55, Application US/09872836
; Publication No. US20040142475A1
; GENERAL INFORMATION:
; APPLICANT: Barman, Shikha P.
; APPLICANT: McKeever, Una
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 08191-018001
; CURRENT APPLICATION NUMBER: US/09/872,836
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,830
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-836-55

Query Match 79.6%; Score 39; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STAPPVHNV 9
| | | | | | | | | |
Db 1 STAPPVHNV 9

RESULT 4
US-10-447-161-97
; Sequence 97, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-97

Query Match 79.6%; Score 39; DB 4; Length 9;

Best Local Similarity 77.8%; Pred. No. 1.7e+06; Mismatches 0; Indels 2; Gaps 0;
Matches 7; Conservative 0;

QY 1 STAPPVHNV 9
Db 1 STAPPAHGV 9

RESULT 5

US-10-296-317-44
; Sequence 44, Application US/10296317
; Publication No. US20040057968A1
; GENERAL INFORMATION:
; APPLICANT: Cel-Sci Corp
; APPLICANT: Zimmerman, Daniel S
; APPLICANT: Savin, Prem S
; TITLE OF INVENTION: T CELL BINDING LIGAND PEPTIDES, PEPTIDE
; FILE REFERENCE: CS-112
; CURRENT APPLICATION NUMBER: US/10/296,317
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/206548
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: PCT/US07/16793
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Muc1 Peptide M1b
US-10-296-317-44

Query Match 79.6%; Score 39; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06; Mismatches 0; Indels 2; Gaps 0;
Matches 7; Conservative 0;

QY 1 STAPPVHNV 9
Db 1 STAPPAHGV 9

RESULT 6

US-10-758-970-55
; Sequence 55, Application US/10758970
; Publication No. US20050037086A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Hsu, Yung-Yueh
; APPLICANT: Tyo, Michael
; TITLE OF INVENTION: CONTINUOUS-FLOW METHOD FOR PREPARING MICROPARTICLES
; FILE REFERENCE: 08191-012001
; CURRENT APPLICATION NUMBER: US/10/758,970
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US/09/715,708A
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/166,516
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-758-970-55

Query Match 79.6%; Score 39; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06; Mismatches 0; Indels 2; Gaps 0;
Matches 7; Conservative 0;

QY 1 STAPPVHNV 9
Db 1 STAPPAHGV 9

Db 1 STAPPAHGV 9

RESULT 7

US-10-751-845-9
; Sequence 9, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiczo, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-751-845-9

Query Match 79.6%; Score 39; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06; Mismatches 0; Indels 2; Gaps 0;
Matches 7; Conservative 0;

QY 1 STAPPVHNV 9
Db 1 STAPPAHGV 9

RESULT 8

US-10-973-927-19
; Sequence 19, Application US/10973927
; Publication No. US20050215501A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Whisnant, John
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING EPITOPE SPREADING
; FILE REFERENCE: C1037.70054US01
; CURRENT APPLICATION NUMBER: US/10/973,927
; CURRENT FILING DATE: 2004-10-25
; PRIOR APPLICATION NUMBER: US 60/514,255
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-973-927-19

Query Match 75.5%; Score 37; DB 5; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06; Mismatches 1; Indels 1; Gaps 0;
Matches 6; Conservative 1;

QY 2 TAPPVHNV 9
Db 1 STPPVHNV 8

RESULT 9
US-09-994-466-10
; Sequence 10, Application US/09994466


```

; Publication No. US20020132771A1
; GENERAL INFORMATION:
; APPLICANT: Madiyalakan, R.
; TITLE OF INVENTION: THERAPEUTIC BINDING AGENTS AGAINST MUC-1 ANTIGEN AND METHODS FOR
; FILE REFERENCE: AREX-P03-002
; CURRENT APPLICATION NUMBER: US/09/994,466
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/724094
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-994-466-10

Query Match      65.3%; Score 32; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPPVHV 7
Db 2 TTAPPAH 8

RESULT 10
US-10-080-013-20
; Sequence 20, Application US/10080013
; Publication No. US2003007248A1
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: US/10/080,013
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-013-20

Query Match      64.3%; Score 31.5; DB 4; Length 8;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 STAPPVHV 9
Db 1 STA-PVHV 8

RESULT 11
US-10-289-566-20
; Sequence 20, Application US/10289566
; Publication No. US20040071571A1
; GENERAL INFORMATION:
; APPLICANT: Leturcq, Didier J.
; APPLICANT: Moriarty, Ann M.
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; APPLICANT: Richards, Jon M.
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT 1342CJP
; CURRENT APPLICATION NUMBER: US/10/289,566
; CURRENT FILING DATE: 2002-11-07

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; PRIOR APPLICATION NUMBER: US 60/270,252
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 10/080,013
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-289-566-20

```

```

Query Match      64.3%; Score 31.5; DB 4; Length 8;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

```

Qy 1 STAPPVHV 9
Db 1 STA-PVHV 8

```

```

RESULT 12
US-09-994-466-7
; Sequence 7, Application US/09994466
; Publication No. US20020132771A1
; GENERAL INFORMATION:
; APPLICANT: Madiyalakan, R.
; TITLE OF INVENTION: THERAPEUTIC BINDING AGENTS AGAINST MUC-1 ANTIGEN AND METHODS FOR
; FILE REFERENCE: AREX-P03-002
; CURRENT APPLICATION NUMBER: US/09/994,466
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/724094
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-994-466-7

```

```

Query Match      63.3%; Score 31; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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Qy 2 TAPPVH 7
Db 1 TAPPAH 6

```

```

RESULT 13
US-11-055-119-3
; Sequence 3, Application US/11055119
; Publication No. US20050142640A1
; GENERAL INFORMATION:
; APPLICANT: Taylor-Papadimitriou, Joyce
; APPLICANT: Heukamp, Lukas Carl
; APPLICANT: Offringa, Rienk
; APPLICANT: Melief, Cornelis Johanna Maria
; APPLICANT: Acres, Bruce
; APPLICANT: Thomas, Mireille
; TITLE OF INVENTION: MUC-1 derived peptides
; FILE REFERENCE: 029395-017
; CURRENT APPLICATION NUMBER: US/11/055,119
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US/09/658,621
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/187,215
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: GB 9921242.5

```


;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: EP 99 40 2237.4
;; PRIOR FILING DATE: 1999-09-10
;; NUMBER OF SEQ ID NOS: 80
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-055-119-3

Query Match 63.3%; Score 31; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPPV 6
|||
Db 4 STAPPV 9

RESULT 14
US-10-334-726-100
;; Sequence 100, Application US/10334726
;; Publication No. US20030211521A1
;; GENERAL INFORMATION:
;; TITLE OF INVENTION: TAYLOR-PAPADIMITROU, JOYCE
;; FILE OF INVENTION: BREAST CANCER ANTIGEN
;; CURRENT APPLICATION NUMBER: US/10/334,726
;; CURRENT FILING DATE: 2003-01-02
;; PRIOR APPLICATION NUMBER: US/09/645,446
;; PRIOR FILING DATE: 2000-08-25
;; PRIOR APPLICATION NUMBER: PCT/GB99/00866
;; PRIOR FILING DATE: 1999-03-19
;; PRIOR APPLICATION NUMBER: GB 9805877.9
;; PRIOR FILING DATE: 1998-09-20
;; NUMBER OF SEQ ID NOS: 324
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 100
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: predicted
US-10-334-726-100

Query Match 57.1%; Score 28; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPVHNV 9
|||
Db 4 PPLHDV 9

RESULT 15
US-09-077-214-28
;; Sequence 28, Application US/09077214
;; Publication No. US20020085997A1
;; GENERAL INFORMATION:
;; APPLICANT: Schmidt, Walter
;; APPLICANT: Birnstiel, Max
;; APPLICANT: Schweighoffer, Tamas
;; APPLICANT: Steinlein, Peter
;; APPLICANT: Buschle, Michael
;; TITLE OF INVENTION: Tumor Vaccine And Process For the
;; PREPARATION THEREOF
;; NUMBER OF SEQUENCES: 33
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
;; STREET: 1100 New York Avenue N.W.
;; CITY: Washington

;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/077,214
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DE 195 43 649.0
;; FILING DATE: 23-NOV-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DE 196 07 044.9
;; FILING DATE: 24-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Flechner, Raz E.
;; REGISTRATION NUMBER: 34,331
;; REFERENCE/DOCKET NUMBER: 0652.1710000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
US-09-077-214-28

Query Match 55.1%; Score 27; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 APPVHNV 9
|||
Db 3 APPQHEI 9

RESULT 16
US-11-055-119-9
;; Sequence 9, Application US/11055119
;; Publication No. US20050142640A1
;; GENERAL INFORMATION:
;; APPLICANT: Taylor-Papadimitriou, Joyce
;; APPLICANT: Heukamp, Lukas Carl
;; APPLICANT: Offringa, Rienk
;; APPLICANT: Melief, Cornelis Johanna Maria
;; APPLICANT: Acres, Bruce
;; APPLICANT: Thomas, Mireille
;; TITLE OF INVENTION: MUC-1 derived peptides
;; FILE REFERENCE: 029395-017
;; CURRENT APPLICATION NUMBER: US/11/055,119
;; CURRENT FILING DATE: 2005-02-11
;; PRIOR APPLICATION NUMBER: US/09/658,621
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: US 60/187,215
;; PRIOR FILING DATE: 2000-03-03
;; PRIOR APPLICATION NUMBER: GB 9921242.5
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: EP 99 40 2237.4
;; PRIOR FILING DATE: 1999-09-10
;; NUMBER OF SEQ ID NOS: 80
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-055-119-9

Query Match 55.1%; Score 27; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPP 5
| | | | |
Db 4 STAPP 8

RESULT 17
US-10-473-127-175
; Sequence 175, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-175

Query Match 53.1%; Score 26; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPVHNV 9
| | | | |
Db 3 PPVNI 8

RESULT 18
US-09-879-936-22
; Sequence 22, Application US/09879936
; Patent No. US20020045564A1
; GENERAL INFORMATION:
; APPLICANT: Van Eyk, Jennifer E.
; APPLICANT: Mak, Alan S.
; APPLICANT: Cote, Graham P.
; TITLE OF INVENTION: Methods of Modulating Muscle Contraction
; FILE REFERENCE: 1997-021-03US
; CURRENT APPLICATION NUMBER: US/09/879,936
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/050,478
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 60/089,505
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: PEPTIDE

; LOCATION: (1) -- (9)
; OTHER INFORMATION: PAK site A autophosphorylation
; NAME/KEY: PEPTIDE
; LOCATION: (9)
; OTHER INFORMATION: Targeted Ser phospho-amino acid
US-09-879-936-22

Query Match 51.0%; Score 25; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 APPVHN 8
| | | | |
Db 2 APPMRN 7

RESULT 19
US-10-001-546-67
; Sequence 67, Application US/10001546
; Publication No. US20030027766A1
; GENERAL INFORMATION:
; APPLICANT: IOANNIDES, CONSTANTIN G.
; APPLICANT: FISK, BRYAN A.
; APPLICANT: IOANNIDES, MARIA G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; TITLE OF INVENTION: T-LYMPHOCYTES
; FILE REFERENCE: UTSC:390USC2
; CURRENT APPLICATION NUMBER: US/10/001,546
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 08/403,459
; PRIOR FILING DATE: 1995-03-14
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-001-546-67

Query Match 51.0%; Score 25; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 STAPPVHNV 9
| | | | |
Db 1 SLADPAHGV 9

RESULT 20
US-10-182-252A-170
; Sequence 170, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31

```
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 170
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-170

Query Match          51.0%; Score 25; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 APPVHV 9
    |||: |
DB 3 APPIQV 9

RESULT 21
US-10-182-252A-172
; Sequence 172, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 172
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-172

Query Match          51.0%; Score 25; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 APPVHV 9
    |||: |
DB 3 APPIQV 9

RESULT 22
US-10-611-440-14
; Sequence 14, Application US/10611440
; Publication No. US20040197912A1
; GENERAL INFORMATION:
; APPLICANT: Berinstein, Neil
; APPLICANT: Gallichan, Scott
; APPLICANT: Lovitt, Corey
; APPLICANT: Parrington, Mark
; APPLICANT: Pedyczak, Artur
; APPLICANT: Radvenyi, Laszlo
; APPLICANT: Singh-Sandhu, Devender
; APPLICANT: Oomen, Raymond P
```

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; APPLICANT: Cao, Shi-Xian
; TITLE OF INVENTION: Tumor Antigens BFA4 and BCV1 for Prevention and/or Treatment of
; FILE REFERENCE: API-02-11-US
; CURRENT APPLICATION NUMBER: US/10/611,440
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/394,346
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/394,503
; PRIOR FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/411,833
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/445,342
; PRIOR FILING DATE: 2003-02-06
; NUMBER OF SEQ ID NOS: 218
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: CLP-2422
US-10-611-440-14

Query Match          51.0%; Score 25; DB 4; Length 9;
Best Local Similarity 56.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PPVHV 9
    |||: |
DB 4 PPLRV 9

RESULT 23
US-09-954-385-198
; Sequence 198, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gascel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzkv, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-198

Query Match          49.0%; Score 24; DB 3; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STAPP 5
    :|||
DB 1 TTAPP 5

RESULT 24
US-10-912-512-198
; Sequence 198, Application US/10912512
; Publication No. US20050042684A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzkzy, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/10/912,512
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US/09/954,385
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-10-912-512-198

Query Match          49.0%; Score 24; DB 5; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STAPP 5
   :||||
Db 1 TTAPP 5

RESULT 25
US-10-235-043-198
; Sequence 198, Application US/10235043
; Publication No. US20050058996A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby M.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzkzy, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-Peptide
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: GC690-2
; CURRENT APPLICATION NUMBER: US/10/235,043
; CURRENT FILING DATE: 2002-09-03
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-10-235-043-198

Query Match          49.0%; Score 24; DB 5; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STAPP 5
   :||||
Db 1 TTAPP 5

US-10-051-411-80
; Publication No. US20040209343A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Draborg, Henriette
; TITLE OF INVENTION: Subtilase variants
; FILE REFERENCE: 10203
; CURRENT APPLICATION NUMBER: US/10/786,850
; CURRENT FILING DATE: 2004-02-24
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patent version 3.2
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Highly mobile region of Savinase
US-10-786-850-33

Query Match          49.0%; Score 24; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 APPVHN 8
   :|||
Db 3 APAAHN 8

RESULT 27
US-11-051-411-80
; Sequence 80, Application US/11051411
; Publication No. US20050196403A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Cheenut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses To
; TITLE OF INVENTION: p53 Using Peptide And Nucleic Acid Compositions
; FILE REFERENCE: 2060.0120000
; CURRENT APPLICATION NUMBER: US/11/051,411
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US/09/458,297
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/017,735
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: PCT/US99/13789
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 09/098,584
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 1492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-80

Query Match          49.0%; Score 24; DB 6; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APPVH 7
   :|||
Db 3 APPQH 7

RESULT 28
US-11-051-411-107
```

```
; Sequence 107, Application US/11051411
; Publication No. US20050196403A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elisa
; TITLE OF INVENTION: Inducing Cellular Immune Responses To
; FILE REFERENCE: 2060.0120000
; CURRENT APPLICATION NUMBER: US/11/051,411
; CURRENT FILING DATE: 2005-02-07
; PRIOR FILING DATE: 1999-12-10
; PRIOR FILING DATE: 1999-12-10
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: PCT/US99/13789
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 09/098,584
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 1492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-107

Query Match          49.0%; Score 24; DB 6; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 APPVH 7
Db      2 APPQH 6

RESULT 29
US-11-051-411-287
; Sequence 287, Application US/11051411
; Publication No. US20050196403A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elisa
; TITLE OF INVENTION: Inducing Cellular Immune Responses To
; FILE REFERENCE: 2060.0120000
; CURRENT APPLICATION NUMBER: US/11/051,411
; CURRENT FILING DATE: 2005-02-07
; PRIOR FILING DATE: 1999-12-10
; PRIOR FILING DATE: 1999-12-10
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: PCT/US99/13789
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 09/098,584
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 1492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 287
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-287

Query Match          49.0%; Score 24; DB 6; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 APPVH 7
Db      3 APPQH 7

RESULT 30
US-11-051-411-496
; Sequence 496, Application US/11051411
; Publication No. US20050196403A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elisa
; TITLE OF INVENTION: Inducing Cellular Immune Responses To
; FILE REFERENCE: 2060.0120000
; CURRENT APPLICATION NUMBER: US/11/051,411
; CURRENT FILING DATE: 2005-02-07
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US/09/458,297
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/017,735
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: PCT/US99/13789
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 09/098,584
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 1492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 496
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-496

Query Match          49.0%; Score 24; DB 6; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 APPVH 7
Db      2 APPQH 6

RESULT 31
US-11-051-411-667
; Sequence 667, Application US/11051411
; Publication No. US20050196403A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elisa
; TITLE OF INVENTION: Inducing Cellular Immune Responses To
; FILE REFERENCE: 2060.0120000
; CURRENT APPLICATION NUMBER: US/11/051,411
```

; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US/09/458,297
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/017,735
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: PCT/US99/13789
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 09/098,584
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 1492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 667
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-667

Query Match 49.0%; Score 24; DB 6; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APPVH 7
||| |
Db 4 APPQH 8

RESULT 32
US-11-051-411-887
; Sequence 887, Application US/11051411
; Publication No. US20050196403A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elisa
; TITLE OF INVENTION: Inducing Cellular Immune Responses To
; FILE REFERENCE: 2060, 0120000
; CURRENT APPLICATION NUMBER: US/11/051,411
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US/09/458,297
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/017,735
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: PCT/US99/13789
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 09/098,584
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 1492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 887
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-887

Query Match 49.0%; Score 24; DB 6; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APPVH 7
||| |
Db 4 APPQH 8

RESULT 33

US-09-932-369A-5
; Sequence 5, Application US/09932369A
; Publication No. US20020123055A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Ganshaw, Grant C.
; APPLICANT: Paech, Christian
; APPLICANT: Paech, Sigrid
; TITLE OF INVENTION: Mass Spectrometric Analysis of
; FILE REFERENCE: GC626-2
; CURRENT APPLICATION NUMBER: US/09/932,369A
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/228,198
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: tryptic co-digest of 15N-subtilisin DAI and
; OTHER INFORMATION: subtilisin
US-09-932-369A-5

Query Match 49.0%; Score 24; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 APPVH 8
||| |
Db 3 APAHN 8

RESULT 34
US-09-833-203-38
; Sequence 38, Application US/09833203
; Publication No. US20030166277A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Smith, Ernest S.
; TITLE OF INVENTION: Targeted Vaccine Delivery Systems
; FILE REFERENCE: 1821,0020001
; CURRENT APPLICATION NUMBER: US/09/833,203
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,472
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: C35 peptides
US-09-833-203-38

Query Match 49.0%; Score 24; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 STAPPVHV 9
| | | |
Db 1 SVAPPPBEV 9

RESULT 35
US-10-809-790-7
; Sequence 7, Application US/10809790
; Publication No. US20040210037A1
; GENERAL INFORMATION:

APPLICANT: Zauderer, Maurice
APPLICANT: Paris, Mark J.
APPLICANT: Smith, Ernest S.
TITLE OF INVENTION: Targeted MHC Class I Alpha3 Vaccine Delivery Systems
FILE REFERENCE: 1843.0120001
CURRENT APPLICATION NUMBER: US/10/809,790
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: US 60/457,896
PRIOR FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-809-790-7

Query Match 49.0%; Score 24; DB 4; Length 9;
Best Local Similarity 55.8%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 STAPPVHV 9
Db 1 SVAPPEEV 9

RESULT 36

US-10-862-195-1350
Sequence 1350, Application US/10862195
Publication No. US20050164324A1
GENERAL INFORMATION:

APPLICANT: GYGI, STEVEN P.
TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
FILE REFERENCE: 58890(70207)
CURRENT APPLICATION NUMBER: US/10/862,195
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 60/476,010
PRIOR FILING DATE: 2003-06-04
NUMBER OF SEQ ID NOS: 2245
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1350
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: See specification as filed for preferred embodiments and description of phosphorylation sites
US-10-862-195-1350

Query Match 49.0%; Score 24; DB 5; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STAPP 5
Db 2 STSPP 6

RESULT 37

US-11-051-411-81
Sequence 81, Application US/11051411
Publication No. US20050196403A1
GENERAL INFORMATION:

APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elisa
TITLE OF INVENTION: Inducing Cellular Immune Responses To
FILE REFERENCE: 2060.0120000

CURRENT APPLICATION NUMBER: US/11/051,411
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US/09/458,297
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/017,735
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: PCT/US99/13789
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 09/098,584
PRIOR FILING DATE: 1998-06-17
NUMBER OF SEQ ID NOS: 1492
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 81
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-11-051-411-81

Query Match 49.0%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APPVH 7
Db 3 APPQH 7

RESULT 38

US-11-051-411-219
Sequence 219, Application US/11051411
Publication No. US20050196403A1
GENERAL INFORMATION:

APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elisa
TITLE OF INVENTION: Inducing Cellular Immune Responses To
FILE REFERENCE: 2060.0120000
CURRENT APPLICATION NUMBER: US/11/051,411
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US/09/458,297
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/017,735
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: PCT/US99/13789
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 09/098,584
PRIOR FILING DATE: 1998-06-17
NUMBER OF SEQ ID NOS: 1492
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 219
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-11-051-411-219

Query Match 49.0%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APPVH 7
Db 2 APPQH 6

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RESULT 39
US-11-051-411-288
; Sequence 288, Application US/11051411
; Publication No. US20050196403A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses To
; TITLE OF INVENTION: p53 Using Peptide And Nucleic Acid Compositions
; FILE REFERENCE: 2060.0120000
; CURRENT APPLICATION NUMBER: US/11/051,411
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US/09/458,297
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/017,735
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: PCT/US99/13789
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 09/098,584
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 1492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-288

Query Match          49.0%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 APPVH 7
Db      3 APPQH 7

RESULT 40
US-11-051-411-368
; Sequence 368, Application US/11051411
; Publication No. US20050196403A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses To
; TITLE OF INVENTION: p53 Using Peptide And Nucleic Acid Compositions
; FILE REFERENCE: 2060.0120000
; CURRENT APPLICATION NUMBER: US/11/051,411
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US/09/458,297
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/017,735
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: PCT/US99/13789
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 09/098,584
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 1492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 9
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-368

Query Match          49.0%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 APPVH 7
Db      1 APPQH 5

RESULT 41
US-11-051-411-544
; Sequence 544, Application US/11051411
; Publication No. US20050196403A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses To
; TITLE OF INVENTION: p53 Using Peptide And Nucleic Acid Compositions
; FILE REFERENCE: 2060.0120000
; CURRENT APPLICATION NUMBER: US/11/051,411
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US/09/458,297
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/017,735
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: PCT/US99/13789
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 09/098,584
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 1492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 544
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-544

Query Match          49.0%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 APPVH 7
Db      1 APPQH 5

RESULT 42
US-11-051-411-557
; Sequence 557, Application US/11051411
; Publication No. US20050196403A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses To
; TITLE OF INVENTION: p53 Using Peptide And Nucleic Acid Compositions
```


FILE REFERENCE: 2060.0120000
CURRENT APPLICATION NUMBER: US/11/051,411
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US/09/458,297
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/017,735
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: PCT/US99/13789
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 09/098,584
PRIOR FILING DATE: 1998-06-17
NUMBER OF SEQ ID NOS: 1492
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 557
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-11-051-411-557

Query Match 49.0%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APPVH 7
|||
Db 3 APPQH 7

RESULT 43
US-11-051-411-733
Sequence 733, Application US/11051411
Publication No. US20050196403A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses To
FILE OF INVENTION: p53 Using Peptide And Nucleic Acid Compositions
FILE REFERENCE: 2060.0120000
CURRENT APPLICATION NUMBER: US/11/051,411
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US/09/458,297
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/017,735
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: PCT/US99/13789
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 09/098,584
PRIOR FILING DATE: 1998-06-17
NUMBER OF SEQ ID NOS: 1492
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 733
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-11-051-411-733

Query Match 49.0%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APPVH 7
|||
Db 2 APPQH 6

RESULT 44
US-11-051-411-817
Sequence 817, Application US/11051411
Publication No. US20050196403A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses To
FILE OF INVENTION: p53 Using Peptide And Nucleic Acid Compositions
FILE REFERENCE: 2060.0120000
CURRENT APPLICATION NUMBER: US/11/051,411
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US/09/458,297
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/017,735
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: PCT/US99/13789
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 09/098,584
PRIOR FILING DATE: 1998-06-17
NUMBER OF SEQ ID NOS: 1492
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 817
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-11-051-411-817

Query Match 49.0%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APPVH 7
|||
Db 5 APPQH 9

RESULT 45
US-11-051-411-939
Sequence 939, Application US/11051411
Publication No. US20050196403A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses To
FILE OF INVENTION: p53 Using Peptide And Nucleic Acid Compositions
FILE REFERENCE: 2060.0120000
CURRENT APPLICATION NUMBER: US/11/051,411
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US/09/458,297
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/017,735
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: PCT/US99/13789
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 09/098,584
PRIOR FILING DATE: 1998-06-17
NUMBER OF SEQ ID NOS: 1492
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 939

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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-939

Query Match          49.0%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APPVH 7
Db 2 APPQH 6

RESULT 46
US-11-051-411-998
; Sequence 998, Application US/11051411
; Publication No. US20050196403A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cellis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses To
; FILE REFERENCE: 2060.0120000
; CURRENT APPLICATION NUMBER: US/11/051,411
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US/09/458,297
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/017,735
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: PCT/US99/13789
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 09/098,584
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 1492
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 998
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-998

Query Match          49.0%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APPVH 7
Db 5 APPQH 9

RESULT 47
US-09-972-035A-9
; Sequence 9, Application US/09972035A
; Patent No. US20020173622A1
; GENERAL INFORMATION:
; APPLICANT: Wettstein, Daniel A
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; TITLE OF INVENTION: Tsg101-GAGp6 INTERACTION AND USE THEREOF
; FILE REFERENCE: 1907.03
; CURRENT APPLICATION NUMBER: US/09/972,035A
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/276,259

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-11-051-411-939

Query Match          49.0%; Score 24; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APPVH 7
Db 5 APPQH 9

RESULT 49
US-10-224-999A-9
; Sequence 9, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-224-999A-9

Query Match          46.9%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAPP 5
Db 2 TAPP 5

RESULT 48
US-10-223-172A-9
; Sequence 9, Application US/10223172A
; Publication No. US2003013844A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Zavitz, Kenton
; APPLICANT: Wettstein, Daniel Albert
; APPLICANT: Morham, Scott
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING HIV INFECTION
; FILE REFERENCE: 5003.01
; CURRENT APPLICATION NUMBER: US/10/223,172A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/313,239
; PRIOR FILING DATE: 2001-08-18
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-223-172A-9

Query Match          46.9%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAPP 5
Db 2 TAPP 5

RESULT 49
US-10-224-999A-9
; Sequence 9, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-224-999A-9
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Query Match 46.9%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAPP 5
DB 2 TAPP 5

RESULT 50
US-10-663-407-9
; Sequence 9, Application US/10663407
; Publication NO. US20040109861A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Incorporated
; APPLICANT: Wettstein, Daniel A
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; TITLE OF INVENTION: TSG101-GAG INTERACTION AND USE THEREOF
; FILE REFERENCE: 1907.04-1
; CURRENT APPLICATION NUMBER: US/10/663,407
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: PCT/US02/08146
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 10/223,172
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 10/224,999
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-663-407-9

Query Match 46.9%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAPP 5
DB 2 TAPP 5

Search completed: February 24, 2006, 10:32:25
Job time : 170 secs

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OM protein - protein search, using sw model

Run on: February 24, 2006, 10:18:31 ; Search time 46 Seconds
(without alignments)
16.176 Million cell updates/sec

Title: US-10-019-513-1
Perfect score: 49
Sequence: 1 STAPPVHV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 111694

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/6 COMB.pdp.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pdp.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	79.6	9	1	US-08-787-547-55
2	39	79.6	9	1	US-08-288-059-19
3	39	79.6	9	2	US-09-593-870A-45
4	39	79.6	9	2	US-09-497-232-1
5	39	79.6	9	2	US-10-296-317-44
6	35	73.5	9	2	US-08-497-232-25
7	35	71.4	9	1	US-08-288-059-17
8	35	71.4	9	1	US-08-288-059-18
9	35	71.4	9	1	US-08-288-059-20
10	35	71.4	9	2	US-09-593-870A-68
11	31	63.3	6	2	US-08-134-198E-23
12	30	61.2	9	1	US-08-288-059-21
13	30	61.2	9	2	US-09-593-870A-67
14	27	55.1	6	2	US-08-134-198E-21
15	27	55.1	6	2	US-08-134-198E-22
16	27	55.1	9	1	US-08-288-059-16
17	27	55.1	9	2	US-09-593-870A-43
18	26	53.1	6	2	US-08-134-198E-24
19	26	53.1	6	2	US-08-134-198E-25
20	26	53.1	7	1	US-08-472-453-4
21	26	53.1	9	1	US-08-288-059-22
22	25	51.0	8	1	US-08-210-266A-1
23	25	51.0	8	1	US-08-210-266A-8
24	25	51.0	8	1	US-08-688-675-1
25	25	51.0	8	1	US-08-688-675-8
26	25	51.0	8	2	US-08-477-860C-1
27	25	51.0	9	2	US-09-100-930A-22

28	25	51.0	9	2	US-08-403-459-67	Sequence 67, Appl
29	24	49.0	6	2	US-08-836-778-1	Sequence 1, Appl
30	24	49.0	7	1	US-08-666-473-24	Sequence 24, Appl
31	24	49.0	8	2	US-08-444-818-340	Sequence 340, Appl
32	24	49.0	9	1	US-08-338-634-16	Sequence 16, Appl
33	24	49.0	9	2	US-09-601-729-98	Sequence 98, Appl
34	24	49.0	9	2	US-09-601-729-102	Sequence 102, Appl
35	23	46.9	6	1	US-08-188-228-1	Sequence 1, Appl
36	23	46.9	6	1	US-08-332-643-1	Sequence 1, Appl
37	23	46.9	6	1	US-08-332-638-1	Sequence 1, Appl
38	23	46.9	6	2	US-09-005-215-29	Sequence 29, Appl
39	23	46.9	6	2	US-09-706-574A-29	Sequence 29, Appl
40	23	46.9	7	2	US-09-192-854-91	Sequence 91, Appl
41	23	46.9	7	2	US-09-511-939-159	Sequence 159, Appl
42	23	46.9	8	1	US-08-615-181-21	Sequence 21, Appl
43	23	46.9	8	1	US-08-615-181-81	Sequence 81, Appl
44	23	46.9	8	2	US-08-477-860C-8	Sequence 8, Appl
45	23	46.9	8	2	US-08-444-818-341	Sequence 341, Appl
46	23	46.9	8	2	US-10-185-815A-76	Sequence 76, Appl
47	23	46.9	9	1	US-07-841-662-31	Sequence 31, Appl
48	23	46.9	9	1	US-08-209-797-31	Sequence 31, Appl
49	23	46.9	9	1	US-08-146-145-19	Sequence 19, Appl
50	23	46.9	9	1	US-08-669-685-31	Sequence 31, Appl
51	23	46.9	9	1	US-08-340-283-34	Sequence 34, Appl
52	23	46.9	9	1	US-08-986-234-63	Sequence 63, Appl
53	23	46.9	9	2	US-09-103-486-31	Sequence 31, Appl
54	23	46.9	9	2	US-08-481-985B-145	Sequence 145, Appl
55	23	46.9	9	2	US-08-501-987-3	Sequence 3, Appl
56	23	46.9	9	2	US-09-039-982A-42	Sequence 42, Appl
57	23	46.9	9	2	US-08-920-413-9	Sequence 9, Appl
58	23	46.9	9	2	US-09-039-641-42	Sequence 42, Appl
59	23	46.9	9	2	US-09-039-762A-42	Sequence 42, Appl
60	23	46.9	9	2	US-09-042-492D-42	Sequence 42, Appl
61	23	46.9	9	2	US-08-197-484-5	Sequence 5, Appl
62	23	46.9	9	2	US-08-137-484-76	Sequence 76, Appl
63	23	46.9	9	2	US-08-913-612A-42	Sequence 42, Appl
64	23	46.9	9	2	US-08-913-612A-48	Sequence 48, Appl
65	23	46.9	9	2	US-09-311-784A-101	Sequence 101, Appl
66	23	46.9	9	2	US-09-389-390-9	Sequence 9, Appl
67	23	46.9	9	2	US-09-454-204A-61	Sequence 61, Appl
68	23	46.9	9	2	US-09-601-729-153	Sequence 153, Appl
69	23	46.9	9	2	US-10-266-463A-42	Sequence 42, Appl
70	23	46.9	9	2	US-10-266-463A-48	Sequence 48, Appl
71	23	46.9	9	4	PCT-US93-01557-31	Sequence 31, Appl
72	23	46.9	9	4	PCT-US95-02121-5	Sequence 5, Appl
73	23	46.9	9	4	PCT-US95-02121-76	Sequence 76, Appl
74	23	46.9	9	4	PCT-US95-04975-16	Sequence 16, Appl
75	23	46.9	9	4	PCT-US95-16415-5	Sequence 5, Appl
76	22	44.9	4	1	US-08-160-317-3	Sequence 3, Appl
77	22	44.9	4	1	US-08-351-147-3	Sequence 3, Appl
78	22	44.9	4	1	US-08-471-154-3	Sequence 3, Appl
79	22	44.9	7	2	US-08-891-271-5	Sequence 5, Appl
80	22	44.9	7	2	US-08-630-915A-203	Sequence 203, Appl
81	22	44.9	7	2	US-09-428-082B-296	Sequence 296, Appl
82	22	44.9	7	2	US-09-879-957-203	Sequence 203, Appl
83	22	44.9	7	2	US-10-394-980-280	Sequence 280, Appl
84	22	44.9	8	2	US-09-011-769A-66	Sequence 66, Appl
85	22	44.9	9	1	US-07-626-589-11	Sequence 11, Appl
86	22	44.9	9	1	US-08-236-410-11	Sequence 11, Appl
87	22	44.9	9	1	US-08-338-634-5	Sequence 5, Appl
88	22	44.9	9	1	US-08-338-634-7	Sequence 7, Appl
89	22	44.9	9	1	US-07-888-943-5	Sequence 5, Appl
90	22	44.9	9	1	US-08-787-547-66	Sequence 66, Appl
91	22	44.9	9	1	US-08-787-547-69	Sequence 69, Appl
92	22	44.9	9	1	US-08-465-421-11	Sequence 11, Appl
93	22	44.9	9	2	US-09-256-194-4	Sequence 4, Appl
94	22	44.9	9	2	US-09-422-375-10	Sequence 10, Appl
95	22	44.9	9	2	US-09-601-729-85	Sequence 85, Appl
96	22	44.9	9	2	US-09-601-729-88	Sequence 88, Appl
97	22	44.9	9	2	US-09-601-729-105	Sequence 105, Appl
98	22	44.9	9	4	PCT-US95-16415-2	Sequence 2, Appl
99	22	44.9	9	4	PCT-US95-16415-3	Sequence 3, Appl
100	21	42.9	5	1	US-08-323-686-6	Sequence 6, Appl

101	21	42.9	9	1	US-08-615-181-35	Sequence 35, Appl	174	19	38.8	8	1	US-08-064-693-7	Sequence 7, Appl
102	21	42.9	9	1	US-08-340-283-51	Sequence 51, Appl	175	19	38.8	8	1	US-08-419-594-3	Sequence 3, Appl
103	21	42.9	9	1	US-08-776-585-15	Sequence 15, Appl	176	19	38.8	8	1	US-08-465-421-12	Sequence 12, Appl
104	21	42.9	9	2	US-09-101-146-20	Sequence 20, Appl	177	19	38.8	8	1	US-08-919-089-3	Sequence 3, Appl
105	20	40.8	4	2	US-09-110-994A-1	Sequence 1, Appl	178	19	38.8	8	1	US-08-340-283-25	Sequence 25, Appl
106	20	40.8	5	1	US-08-325-509-49	Sequence 49, Appl	179	19	38.8	8	2	US-08-444-818-342	Sequence 342, Appl
107	20	40.8	5	1	US-08-477-509B-3	Sequence 3, Appl	180	19	38.8	8	2	US-08-444-818-343	Sequence 343, Appl
108	20	40.8	5	2	US-08-482-085B-3	Sequence 3, Appl	181	19	38.8	8	2	US-08-444-818-676	Sequence 676, Appl
109	20	40.8	5	2	US-09-444-731A-3	Sequence 3, Appl	182	19	38.8	8	2	US-09-100-930A-19	Sequence 19, Appl
110	20	40.8	5	2	US-09-119-507B-4	Sequence 4, Appl	183	19	38.8	8	2	US-08-885-366-7	Sequence 7, Appl
111	20	40.8	5	2	US-08-897-556A-4	Sequence 4, Appl	184	19	38.8	8	2	US-09-314-268-22	Sequence 22, Appl
112	20	40.8	5	2	US-08-547-693-4	Sequence 4, Appl	185	19	38.8	8	2	US-09-314-268-23	Sequence 23, Appl
113	20	40.8	6	2	US-08-134-198E-20	Sequence 20, Appl	186	19	38.8	8	2	US-09-314-268-24	Sequence 24, Appl
114	20	40.8	6	2	US-09-486-356-24	Sequence 24, Appl	187	19	38.8	8	2	US-09-314-268-25	Sequence 25, Appl
115	20	40.8	6	2	US-09-636-252A-14	Sequence 14, Appl	188	19	38.8	8	2	US-09-314-268-26	Sequence 26, Appl
116	20	40.8	6	2	US-09-577-528B-24	Sequence 24, Appl	189	19	38.8	8	2	US-08-695-692B-21	Sequence 21, Appl
117	20	40.8	6	2	US-10-208-557-24	Sequence 24, Appl	190	19	38.8	8	2	US-09-239-043D-8	Sequence 8, Appl
118	20	40.8	6	2	US-10-317-252B-403	Sequence 403, App	191	19	38.8	8	2	US-09-239-043D-201	Sequence 201, App
119	20	40.8	7	1	US-08-472-453-57	Sequence 57, Appl	192	19	38.8	8	2	US-09-239-043D-1326	Sequence 1326, App
120	20	40.8	7	2	US-08-301-435-62	Sequence 62, Appl	193	19	38.8	8	2	US-09-437-136-6	Sequence 6, Appl
121	20	40.8	7	2	US-09-731-242A-22	Sequence 22, Appl	194	19	38.8	8	2	US-09-693-746-165	Sequence 165, App
122	20	40.8	7	4	PCT-US95-10904-62	Sequence 62, Appl	195	19	38.8	8	2	US-10-181-546-1	Sequence 1, Appl
123	20	40.8	8	2	US-08-444-818-339	Sequence 33, App	196	19	38.8	8	2	US-09-788-308E-4	Sequence 4, Appl
124	20	40.8	9	1	US-08-417-174-14	Sequence 14, Appl	197	19	38.8	8	2	US-10-655-201-6	Sequence 6, Appl
125	20	40.8	9	1	US-08-231-565A-14	Sequence 14, Appl	198	19	38.8	8	4	PCT-US93-04754-7	Sequence 7, Appl
126	20	40.8	9	1	US-09-007-961-14	Sequence 14, Appl	199	19	38.8	8	6	5171845-8	Patent No. 5171845
127	20	40.8	9	2	US-09-101-146-36	Sequence 36, Appl	200	19	38.8	8	6	5175147-10	Patent No. 5175147
128	20	40.8	9	2	US-09-258-754-249	Sequence 249, App	201	19	38.8	9	1	US-08-470-179-103	Sequence 103, App
129	20	40.8	9	2	US-09-042-107-249	Sequence 24, App	202	19	38.8	9	1	US-08-214-650-43	Sequence 43, Appl
130	20	40.8	9	2	US-09-267-439-14	Sequence 14, Appl	203	19	38.8	9	1	US-08-615-181-18	Sequence 18, Appl
131	20	40.8	9	2	US-09-073-138-14	Sequence 14, Appl	204	19	38.8	9	1	US-08-615-181-96	Sequence 96, Appl
132	20	40.8	9	2	US-09-722-250D-249	Sequence 249, App	205	19	38.8	9	1	US-08-230-268-17	Sequence 17, Appl
133	20	40.8	9	2	US-09-676-475A-249	Sequence 249, App	206	19	38.8	9	1	US-08-340-283-18	Sequence 18, Appl
134	20	40.8	9	2	US-09-623-548A-1346	Sequence 7, Appl	207	19	38.8	9	1	US-08-340-283-144	Sequence 144, App
135	20	40.8	9	2	US-09-935-430-7	Sequence 1346, Ap	208	19	38.8	9	1	US-08-146-028-447	Sequence 447, App
136	20	40.8	9	2	US-09-657-276-1346	Sequence 1346, Ap	209	19	38.8	9	1	US-08-146-028-448	Sequence 448, App
137	20	40.8	9	2	US-09-716-964B-9	Sequence 9, Appl	210	19	38.8	9	1	US-08-146-028-449	Sequence 449, App
138	20	40.8	9	2	US-10-607-595-249	Sequence 249, App	211	19	38.8	9	1	US-08-146-028-450	Sequence 450, App
139	20	40.8	9	2	US-09-641-808-16	Sequence 16, Appl	212	19	38.8	9	1	US-08-146-028-451	Sequence 451, App
140	19	38.8	5	2	US-09-006-428A-22	Sequence 22, Appl	213	19	38.8	9	1	US-08-146-028-452	Sequence 452, App
141	19	38.8	5	2	US-08-433-441A-8	Sequence 8, Appl	214	19	38.8	9	1	US-08-350-260A-480	Sequence 480, App
142	19	38.8	5	2	US-08-433-441A-9	Sequence 9, Appl	215	19	38.8	9	2	US-08-723-425A-447	Sequence 447, App
143	19	38.8	5	2	US-09-615-387C-22	Sequence 22, Appl	216	19	38.8	9	2	US-08-723-425A-448	Sequence 448, App
144	19	38.8	5	2	US-09-807-063-30	Sequence 30, Appl	217	19	38.8	9	2	US-08-723-425A-449	Sequence 449, App
145	19	38.8	6	1	US-08-089-994A-9	Sequence 9, Appl	218	19	38.8	9	2	US-08-723-425A-450	Sequence 450, App
146	19	38.8	6	1	US-08-078-812-134	Sequence 134, App	219	19	38.8	9	2	US-08-723-425A-451	Sequence 451, App
147	19	38.8	6	1	US-08-487-006-49	Sequence 49, Appl	220	19	38.8	9	2	US-08-723-425A-452	Sequence 452, App
148	19	38.8	6	1	US-08-488-659A-49	Sequence 49, Appl	221	19	38.8	9	2	US-09-112-206-447	Sequence 447, App
149	19	38.8	6	2	US-08-134-198E-26	Sequence 26, Appl	222	19	38.8	9	2	US-09-112-206-448	Sequence 448, App
150	19	38.8	6	2	US-09-636-252A-15	Sequence 15, Appl	223	19	38.8	9	2	US-09-112-206-449	Sequence 449, App
151	19	38.8	6	2	US-09-006-428A-21	Sequence 21, Appl	224	19	38.8	9	2	US-09-112-206-450	Sequence 450, App
152	19	38.8	6	2	US-09-615-387C-21	Sequence 21, Appl	225	19	38.8	9	2	US-09-112-206-451	Sequence 451, App
153	19	38.8	6	2	US-09-657-276-1217	Sequence 1217, Ap	226	19	38.8	9	2	US-09-112-206-452	Sequence 452, App
154	19	38.8	6	2	US-09-657-276-1217	Sequence 1217, Ap	227	19	38.8	9	2	US-09-227-357-312	Sequence 312, App
155	19	38.8	6	2	US-09-788-308E-1	Sequence 1, Appl	228	19	38.8	9	2	US-09-023-905A-20	Sequence 20, Appl
156	19	38.8	6	2	US-10-317-252B-392	Sequence 392, App	229	19	38.8	9	2	US-09-023-905A-38	Sequence 38, Appl
157	19	38.8	6	2	US-10-317-252B-393	Sequence 393, App	230	19	38.8	9	2	US-09-104-337A-480	Sequence 480, App
158	19	38.8	6	4	PCT-US94-07605-9	Sequence 9, Appl	231	19	38.8	9	2	US-09-311-784A-370	Sequence 370, App
159	19	38.8	7	1	US-08-201-046A-12	Sequence 12, Appl	232	19	38.8	9	2	US-09-311-784A-404	Sequence 404, App
160	19	38.8	7	1	US-08-545-228-1	Sequence 1, Appl	233	19	38.8	9	2	US-09-344-040C-20	Sequence 20, Appl
161	19	38.8	7	1	US-08-666-473-28	Sequence 28, Appl	234	19	38.8	9	2	US-08-801-405B-4	Sequence 4, Appl
162	19	38.8	7	2	US-08-946-329A-23	Sequence 23, Appl	235	19	38.8	9	2	US-09-508-930D-14	Sequence 14, Appl
163	19	38.8	7	2	US-08-567-357A-23	Sequence 23, Appl	236	19	38.8	9	2	US-09-790-497A-395	Sequence 395, App
164	19	38.8	7	2	US-08-729-743A-23	Sequence 23, Appl	237	19	38.8	9	2	US-09-790-497A-396	Sequence 396, App
165	19	38.8	7	2	US-09-084-605B-12	Sequence 12, Appl	238	19	38.8	9	2	US-09-790-497A-397	Sequence 397, App
166	19	38.8	7	2	US-09-084-605B-27	Sequence 27, Appl	239	19	38.8	9	2	US-09-790-497A-398	Sequence 398, App
167	19	38.8	7	2	US-09-794-960-6	Sequence 6, Appl	240	19	38.8	9	2	US-09-790-497A-399	Sequence 399, App
168	19	38.8	7	2	US-09-508-930D-11	Sequence 11, Appl	241	19	38.8	9	2	US-09-790-497A-400	Sequence 400, App
169	19	38.8	7	2	US-09-562-914-23	Sequence 23, Appl	242	19	38.8	9	2	US-09-790-497A-576	Sequence 576, App
170	19	38.8	8	1	US-07-626-589-12	Sequence 12, Appl	243	19	38.8	9	2	US-09-576-824A-395	Sequence 395, App
171	19	38.8	8	1	US-08-072-063-7	Sequence 7, Appl	244	19	38.8	9	2	US-09-576-824A-396	Sequence 396, App
172	19	38.8	8	1	US-08-323-444A-5	Sequence 5, Appl	245	19	38.8	9	2	US-09-576-824A-397	Sequence 397, App
173	19	38.8	8	1	US-08-236-410-12	Sequence 12, Appl	246	19	38.8	9	2	US-09-576-824A-398	Sequence 398, App

247	19	38.8	9	2	US-09-576-824A-399	Sequence 399, App	320	18	36.7	5	2	US-09-823-240A-4	Sequence 4, Appli
248	19	38.8	9	2	US-09-576-824A-400	Sequence 400, App	321	18	36.7	5	2	US-09-095-639A-1	Sequence 1, Appli
249	19	38.8	9	2	US-09-833-039A-20	Sequence 20, Appli	322	18	36.7	5	2	US-09-608-892-35	Sequence 35, Appli
250	19	38.8	9	2	US-09-239-043D-541	Sequence 541, App	323	18	36.7	5	2	US-10-346-927-27	Sequence 27, Appli
251	19	38.8	9	2	US-09-239-043D-1350	Sequence 1350, Ap	324	18	36.7	5	2	US-10-346-927-85	Sequence 85, Appli
252	19	38.8	9	2	US-09-239-043D-1779	Sequence 1779, Ap	325	18	36.7	5	4	PCT-US94-01840-13	Sequence 13, Appli
253	19	38.8	9	2	US-09-239-043D-1831	Sequence 1831, Ap	326	18	36.7	5	4	PCT-US94-02552-12	Sequence 12, Appli
254	19	38.8	9	2	US-09-239-043D-1933	Sequence 1933, Ap	327	18	36.7	6	1	US-07-989-290-2	Sequence 2, Appli
255	19	38.8	9	2	US-09-680-497-447	Sequence 447, App	328	18	36.7	6	1	US-08-271-698-2	Sequence 2, Appli
256	19	38.8	9	2	US-09-680-497-448	Sequence 448, App	329	18	36.7	6	1	US-08-171-737-18	Sequence 18, Appli
257	19	38.8	9	2	US-09-680-497-449	Sequence 449, App	330	18	36.7	6	1	US-08-117-491-16	Sequence 16, Appli
258	19	38.8	9	2	US-09-680-497-450	Sequence 450, App	331	18	36.7	6	1	US-08-014-979-88	Sequence 88, Appli
259	19	38.8	9	2	US-09-680-497-451	Sequence 451, App	332	18	36.7	6	1	US-08-201-046A-6	Sequence 6, Appli
260	19	38.8	9	2	US-09-680-497-452	Sequence 452, App	333	18	36.7	6	1	US-08-468-596-2	Sequence 2, Appli
261	19	38.8	9	2	US-09-408-036B-28	Sequence 28, Appli	334	18	36.7	6	1	US-08-299-636-38	Sequence 38, Appli
262	19	38.8	9	2	US-09-367-703B-5	Sequence 5, Appli	335	18	36.7	6	1	US-08-279-155-37	Sequence 37, Appli
263	19	38.8	9	2	US-09-935-430-11	Sequence 11, Appli	336	18	36.7	6	1	US-08-271-364A-16	Sequence 16, Appli
264	19	38.8	9	2	US-09-935-430-467	Sequence 467, App	337	18	36.7	6	1	US-08-703-988A-37	Sequence 37, Appli
265	19	38.8	9	2	US-09-935-430-552	Sequence 552, App	338	18	36.7	6	1	US-08-209-261B-6	Sequence 6, Appli
266	19	38.8	9	2	US-09-685-010-39	Sequence 39, Appli	339	18	36.7	6	1	US-08-478-386A-64	Sequence 64, Appli
267	19	38.8	9	2	US-09-685-010-43	Sequence 43, Appli	340	18	36.7	6	1	US-08-472-453-11	Sequence 11, Appli
268	19	38.8	9	2	US-09-065-902-17	Sequence 17, Appli	341	18	36.7	6	1	US-08-472-453-16	Sequence 16, Appli
269	19	38.8	9	2	US-09-978-309A-39	Sequence 39, Appli	342	18	36.7	6	1	US-08-472-453-18	Sequence 18, Appli
270	19	38.8	9	2	US-09-978-309A-43	Sequence 43, Appli	343	18	36.7	6	1	US-08-472-453-19	Sequence 19, Appli
271	19	38.8	9	2	US-09-973-278-297	Sequence 297, App	344	18	36.7	6	1	US-08-472-453-28	Sequence 28, Appli
272	19	38.8	9	2	US-09-641-808-14	Sequence 14, Appli	345	18	36.7	6	1	US-08-472-453-28	Sequence 40, Appli
273	18	36.7	4	1	US-08-544-143A-22	Sequence 22, Appli	346	18	36.7	6	1	US-08-472-453-42	Sequence 42, Appli
274	18	36.7	4	1	US-08-477-509B-12	Sequence 12, Appli	347	18	36.7	6	1	US-08-472-453-50	Sequence 50, Appli
275	18	36.7	4	2	US-08-482-085B-12	Sequence 12, Appli	348	18	36.7	6	1	US-08-472-453-53	Sequence 53, Appli
276	18	36.7	4	2	US-08-904-760B-24	Sequence 24, Appli	349	18	36.7	6	1	US-08-292-597-64	Sequence 64, Appli
277	18	36.7	4	2	US-09-444-791A-12	Sequence 12, Appli	350	18	36.7	6	1	US-08-222-715B-16	Sequence 16, Appli
278	18	36.7	4	2	US-09-547-693-178	Sequence 178, App	351	18	36.7	6	1	US-08-666-473-108	Sequence 108, App
279	18	36.7	4	2	US-09-547-693-214	Sequence 214, App	352	18	36.7	6	1	US-08-360-784B-36	Sequence 36, Appli
280	18	36.7	4	2	US-09-095-639A-7	Sequence 7, Appli	353	18	36.7	6	1	US-08-388-653-64	Sequence 64, Appli
281	18	36.7	4	2	US-09-825-561A-70	Sequence 70, Appli	354	18	36.7	6	1	US-08-473-985-64	Sequence 64, Appli
282	18	36.7	4	2	US-10-185-815A-99	Sequence 99, Appli	355	18	36.7	6	1	US-08-612-842-37	Sequence 37, Appli
283	18	36.7	5	1	US-08-171-737-2	Sequence 2, Appli	356	18	36.7	6	1	US-08-483-898-64	Sequence 64, Appli
284	18	36.7	5	1	US-08-202-178-2	Sequence 2, Appli	357	18	36.7	6	2	US-09-087-716-64	Sequence 64, Appli
285	18	36.7	5	1	US-08-299-636-37	Sequence 37, Appli	358	18	36.7	6	2	US-08-944-479-11	Sequence 11, Appli
286	18	36.7	5	1	US-08-279-155-36	Sequence 36, Appli	359	18	36.7	6	2	US-09-054-308A-36	Sequence 36, Appli
287	18	36.7	5	1	US-08-713-484-2	Sequence 2, Appli	360	18	36.7	6	2	US-09-157-753-64	Sequence 64, Appli
288	18	36.7	5	1	US-08-477-509B-13	Sequence 13, Appli	361	18	36.7	6	2	US-09-157-753-64	Sequence 64, Appli
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291	18	36.7	5	1	US-08-454-859-1	Sequence 1, Appli	364	18	36.7	6	2	US-08-819-101-11	Sequence 11, Appli
292	18	36.7	5	1	US-08-472-453-27	Sequence 27, Appli	365	18	36.7	6	2	US-08-904-760B-26	Sequence 26, Appli
293	18	36.7	5	1	US-08-666-473-6	Sequence 6, Appli	366	18	36.7	6	2	US-08-158-010-64	Sequence 64, Appli
294	18	36.7	5	1	US-08-666-473-10	Sequence 10, Appli	367	18	36.7	6	2	US-09-087-647-64	Sequence 64, Appli
295	18	36.7	5	1	US-08-340-283-3	Sequence 3, Appli	368	18	36.7	6	2	US-08-602-999A-249	Sequence 249, App
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297	18	36.7	5	1	US-08-955-263-2	Sequence 12, Appli	370	18	36.7	6	2	US-09-302-629-64	Sequence 64, Appli
298	18	36.7	5	1	US-08-612-842-36	Sequence 36, Appli	371	18	36.7	6	2	US-09-295-996B-12	Sequence 12, Appli
299	18	36.7	5	2	US-08-915-189-27	Sequence 27, Appli	372	18	36.7	6	2	US-09-500-124-249	Sequence 249, App
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301	18	36.7	5	2	US-08-972-760-27	Sequence 27, Appli	374	18	36.7	6	2	US-09-295-846B-15	Sequence 15, Appli
302	18	36.7	5	2	US-08-972-760-85	Sequence 85, Appli	375	18	36.7	6	2	US-09-551-737C-15	Sequence 15, Appli
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304	18	36.7	5	2	US-08-904-760B-25	Sequence 25, Appli	377	18	36.7	6	2	US-09-295-924B-2	Sequence 2, Appli
305	18	36.7	5	2	US-09-089-645A-27	Sequence 27, Appli	378	18	36.7	6	2	US-09-520-254-11	Sequence 11, Appli
306	18	36.7	5	2	US-09-089-645A-85	Sequence 85, Appli	379	18	36.7	6	2	US-09-551-738B-12	Sequence 12, Appli
307	18	36.7	5	2	US-08-810-712-12	Sequence 12, Appli	380	18	36.7	6	2	US-09-599-287A-3	Sequence 3, Appli
308	18	36.7	5	2	US-09-503-998-27	Sequence 27, Appli	381	18	36.7	6	2	US-09-599-287A-19	Sequence 19, Appli
309	18	36.7	5	2	US-09-503-998-85	Sequence 85, Appli	382	18	36.7	6	2	US-09-547-693-171	Sequence 171, App
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311	18	36.7	5	2	US-09-373-694-27	Sequence 27, Appli	384	18	36.7	6	2	US-09-790-497A-598	Sequence 598, App
312	18	36.7	5	2	US-09-436-874-11	Sequence 11, Appli	385	18	36.7	6	2	US-09-428-082B-324	Sequence 324, App
313	18	36.7	5	2	US-09-119-507B-6	Sequence 6, Appli	386	18	36.7	6	2	US-09-576-824A-443	Sequence 443, App
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316	18	36.7	5	2	US-09-939-481-85	Sequence 85, Appli	389	18	36.7	6	2	US-10-062-623B-26	Sequence 26, Appli
317	18	36.7	5	2	US-08-817-832B-11	Sequence 11, Appli	390	18	36.7	6	2	US-09-454-651B-26	Sequence 26, Appli
318	18	36.7	5	2	US-08-877-605-294	Sequence 294, App	391	18	36.7	6	2	US-09-454-651B-27	Sequence 27, Appli
319	18	36.7	5	2	US-09-547-693-6	Sequence 6, Appli	392	18	36.7	6	2	US-09-454-651B-31	Sequence 31, Appli

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396	18	36.7	6	2	US-10-078-547-19	Sequence 19, Appl	469	18	36.7	7	2	US-09-520-254-8	Sequence 8, Appl
397	18	36.7	6	2	US-10-281-652-13	Sequence 13, Appl	470	18	36.7	7	2	US-09-551-738B-13	Sequence 9, Appl
398	18	36.7	6	2	US-09-688-017-131	Sequence 131, App	471	18	36.7	7	2	US-09-551-738B-13	Sequence 13, Appl
399	18	36.7	7	1	US-07-989-290-3	Sequence 3, Appl	472	18	36.7	7	2	US-09-599-287A-26	Sequence 26, Appl
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401	18	36.7	7	1	US-08-271-698-3	Sequence 3, Appl	474	18	36.7	7	2	US-09-931-552-36	Sequence 36, Appl
402	18	36.7	7	1	US-08-151-219-3	Sequence 3, Appl	475	18	36.7	7	2	US-08-861-153A-48	Sequence 48, Appl
403	18	36.7	7	1	US-08-468-596-3	Sequence 3, Appl	476	18	36.7	7	2	US-09-731-242A-19	Sequence 19, Appl
404	18	36.7	7	1	US-08-188-223-10	Sequence 10, Appl	477	18	36.7	7	2	US-09-731-242A-21	Sequence 21, Appl
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411	18	36.7	7	1	US-08-472-453-14	Sequence 14, Appl	484	18	36.7	7	2	US-10-078-547-26	Sequence 26, Appl
412	18	36.7	7	1	US-08-472-453-18	Sequence 38, Appl	485	18	36.7	7	2	US-09-688-017-132	Sequence 132, App
413	18	36.7	7	1	US-08-472-453-39	Sequence 39, Appl	486	18	36.7	7	2	US-09-902-481B-12	Sequence 12, Appl
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419	18	36.7	7	1	US-08-666-473-7	Sequence 7, Appl	492	18	36.7	8	1	US-08-271-698-4	Sequence 4, Appl
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421	18	36.7	7	1	US-08-893-853-20	Sequence 20, Appl	494	18	36.7	8	1	US-08-202-178-4	Sequence 4, Appl
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426	18	36.7	7	2	US-08-944-479-8	Sequence 8, Appl	499	18	36.7	8	1	US-08-713-484-4	Sequence 4, Appl
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430	18	36.7	7	2	US-08-771-986A-13	Sequence 13, Appl	503	18	36.7	8	1	US-08-955-263-4	Sequence 4, Appl
431	18	36.7	7	2	US-08-819-101-6	Sequence 6, Appl	504	18	36.7	8	1	US-08-654-604-14	Sequence 14, Appl
432	18	36.7	7	2	US-08-819-101-8	Sequence 8, Appl	505	18	36.7	8	1	US-08-654-604-15	Sequence 15, Appl
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438	18	36.7	7	2	US-09-113-921-50	Sequence 50, Appl	511	18	36.7	8	2	US-08-873-970-19	Sequence 19, Appl
439	18	36.7	7	2	US-08-640-737-35	Sequence 35, Appl	512	18	36.7	8	2	US-08-477-860C-6	Sequence 6, Appl
440	18	36.7	7	2	US-09-103-478-5	Sequence 5, Appl	513	18	36.7	8	2	US-08-817-547A-24	Sequence 24, Appl
441	18	36.7	7	2	US-09-103-478-17	Sequence 17, Appl	514	18	36.7	8	2	US-08-246-441-8	Sequence 8, Appl
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456	18	36.7	7	2	US-09-073-541A-41	Sequence 41, Appl	529	18	36.7	8	2	US-09-295-996B-10	Sequence 10, Appl
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460	18	36.7	7	2	US-09-026-221-17	Sequence 17, Appl	533	18	36.7	8	2	US-09-422-375-9	Sequence 9, Appl
461	18	36.7	7	2	US-09-076-372-3	Sequence 3, Appl	534	18	36.7	8	2	US-08-488-446-491	Sequence 491, App
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540	18	36.7	8	2	US-09-295-924B-4	Sequence 4, Appl1	613	18	36.7	9	2	US-08-817-547A-23	Sequence 23, Appl
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543	18	36.7	8	2	US-08-475-955-195	Sequence 195, Appl	616	18	36.7	9	2	US-08-723-425A-433	Sequence 433, Appl
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553	18	36.7	8	2	US-09-239-043D-397	Sequence 397, Appl	626	18	36.7	9	2	US-09-112-206-434	Sequence 434, Appl
554	18	36.7	8	2	US-09-239-043D-308	Sequence 308, Appl	627	18	36.7	9	2	US-09-112-206-435	Sequence 435, Appl
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558	18	36.7	8	2	US-10-062-623B-28	Sequence 28, Appl	631	18	36.7	9	2	US-09-112-206-439	Sequence 439, Appl
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565	18	36.7	8	2	US-07-867-819D-146	Sequence 146, Appl	638	18	36.7	9	2	US-09-105-839D-65	Sequence 65, Appl
566	18	36.7	8	2	US-09-756-283A-54	Sequence 54, Appl	639	18	36.7	9	2	US-08-997-802-10	Sequence 10, Appl
567	18	36.7	8	2	US-09-688-017-133	Sequence 133, Appl	640	18	36.7	9	2	US-08-997-802-11	Sequence 11, Appl
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573	18	36.7	9	1	US-08-615-181-29	Sequence 29, Appl	646	18	36.7	9	2	US-09-073-138-13	Sequence 13, Appl
574	18	36.7	9	1	US-08-615-181-91	Sequence 91, Appl	647	18	36.7	9	2	US-09-344-040C-86	Sequence 86, Appl
575	18	36.7	9	1	US-08-615-181-97	Sequence 97, Appl	648	18	36.7	9	2	US-09-344-040C-86	Sequence 86, Appl
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577	18	36.7	9	1	US-08-703-988A-38	Sequence 38, Appl	650	18	36.7	9	2	US-09-295-924B-9	Sequence 9, Appl1
578	18	36.7	9	1	US-08-592-294-3	Sequence 3, Appl1	651	18	36.7	9	2	US-09-543-608A-22	Sequence 22, Appl
579	18	36.7	9	1	US-08-408-604A-87	Sequence 87, Appl	652	18	36.7	9	2	US-10-012-542-386	Sequence 386, Appl
580	18	36.7	9	1	US-08-454-859-2	Sequence 2, Appl1	653	18	36.7	9	2	US-09-790-497A-381	Sequence 381, Appl
581	18	36.7	9	1	US-08-666-473-111	Sequence 111, Appl	654	18	36.7	9	2	US-09-790-497A-382	Sequence 382, Appl
582	18	36.7	9	1	US-08-666-473-112	Sequence 112, Appl	655	18	36.7	9	2	US-09-790-497A-383	Sequence 383, Appl
583	18	36.7	9	1	US-08-244-951A-7	Sequence 7, Appl1	656	18	36.7	9	2	US-09-790-497A-384	Sequence 384, Appl
584	18	36.7	9	1	US-08-417-174-13	Sequence 13, Appl	657	18	36.7	9	2	US-09-790-497A-385	Sequence 385, Appl
585	18	36.7	9	1	US-08-765-179B-17	Sequence 17, Appl	658	18	36.7	9	2	US-09-790-497A-386	Sequence 386, Appl
586	18	36.7	9	1	US-07-828-789-4	Sequence 4, Appl1	659	18	36.7	9	2	US-09-790-497A-387	Sequence 387, Appl
587	18	36.7	9	1	US-07-828-789-12	Sequence 12, Appl	660	18	36.7	9	2	US-09-790-497A-401	Sequence 401, Appl
588	18	36.7	9	1	US-08-389-011-5	Sequence 5, Appl1	661	18	36.7	9	2	US-09-790-497A-566	Sequence 566, Appl
589	18	36.7	9	1	US-08-340-283-11	Sequence 11, Appl	662	18	36.7	9	2	US-09-790-497A-567	Sequence 567, Appl
590	18	36.7	9	1	US-08-340-283-13	Sequence 13, Appl	663	18	36.7	9	2	US-09-790-497A-568	Sequence 568, Appl
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592	18	36.7	9	1	US-08-340-283-134	Sequence 134, Appl	665	18	36.7	9	2	US-09-790-497A-570	Sequence 570, Appl
593	18	36.7	9	1	US-08-340-283-141	Sequence 141, Appl	666	18	36.7	9	2	US-09-790-497A-571	Sequence 571, Appl
594	18	36.7	9	1	US-08-231-565A-13	Sequence 13, Appl	667	18	36.7	9	2	US-09-576-824A-381	Sequence 381, Appl
595	18	36.7	9	1	US-08-146-028-433	Sequence 433, Appl	668	18	36.7	9	2	US-09-576-824A-382	Sequence 382, Appl
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603	18	36.7	9	1	US-08-893-853-56	Sequence 56, Appl	676	18	36.7	9	2	US-09-833-039A-107	Sequence 107, Appl
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608	18	36.7	9	1	US-08-612-842-38	Sequence 38, Appl	681	18	36.7	9	2	US-09-239-043D-398	Sequence 398, Appl
609	18	36.7	9	1	US-08-986-234-77	Sequence 77, Appl	682	18	36.7	9	2	US-09-239-043D-414	Sequence 414, Appl
610	18	36.7	9	1	US-09-007-961-13	Sequence 13, Appl	683	18	36.7	9	2	US-09-239-043D-923	Sequence 923, Appl
611	18	36.7	9	2	US-08-369-643-59	Sequence 59, Appl	684	18	36.7	9	2		

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686	18	36.7	9	2	US-09-239-043D-2344	Sequence 2344, Ap	759	17	34.7	7	2	US-09-731-242A-17	Sequence 17, Appl
687	18	36.7	9	2	US-09-239-043D-2403	Sequence 2403, Ap	760	17	34.7	7	2	US-09-731-242A-20	Sequence 20, Appl
688	18	36.7	9	2	US-09-680-497-433	Sequence 433, Ap	761	17	34.7	7	2	US-10-042-991-1	Sequence 1, Appl
689	18	36.7	9	2	US-09-680-497-434	Sequence 434, Ap	762	17	34.7	7	2	US-09-723-257-50	Sequence 50, Appl
690	18	36.7	9	2	US-09-680-497-435	Sequence 435, Ap	763	17	34.7	7	2	US-10-038-937-8	Sequence 8, Appl
691	18	36.7	9	2	US-09-680-497-436	Sequence 436, Ap	764	17	34.7	7	2	US-10-007-747-8	Sequence 8, Appl
692	18	36.7	9	2	US-09-680-497-437	Sequence 437, Ap	765	17	34.7	7	2	US-09-884-767A-104	Sequence 104, App
693	18	36.7	9	2	US-09-680-497-438	Sequence 438, Ap	766	17	34.7	7	2	US-09-772-819-44	Sequence 44, Appl
694	18	36.7	9	2	US-09-680-497-439	Sequence 439, Ap	767	17	34.7	7	2	US-09-945-901-8	Sequence 8, Appl
695	18	36.7	9	2	US-09-680-497-453	Sequence 453, Ap	768	17	34.7	7	2	US-10-150-262A-11	Sequence 11, Appl
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697	18	36.7	9	2	US-10-115-123-386	Sequence 386, Ap	770	17	34.7	8	1	US-08-057-167-7	Sequence 7, Appl
698	18	36.7	9	2	US-10-121-857-17	Sequence 17, Appl	771	17	34.7	8	1	US-08-256-236-7	Sequence 7, Appl
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701	18	36.7	9	2	US-09-935-430-15	Sequence 15, Appl	774	17	34.7	8	1	US-08-208-181A-4	Sequence 4, Appl
702	18	36.7	9	2	US-09-935-430-43	Sequence 43, Appl	775	17	34.7	8	1	US-08-459-064B-14	Sequence 14, Appl
703	18	36.7	9	2	US-09-935-430-235	Sequence 235, Ap	776	17	34.7	8	1	US-08-459-064B-31	Sequence 31, Appl
704	18	36.7	9	2	US-09-935-430-314	Sequence 314, Ap	777	17	34.7	8	1	US-08-459-064B-31	Sequence 31, Appl
705	18	36.7	9	2	US-09-935-430-478	Sequence 478, Ap	778	17	34.7	8	1	US-08-460-421A-14	Sequence 14, Appl
706	18	36.7	9	2	US-09-865-548A-48	Sequence 48, Appl	779	17	34.7	8	1	US-08-460-421A-31	Sequence 31, Appl
707	18	36.7	9	2	US-09-865-548A-60	Sequence 60, Appl	780	17	34.7	8	1	US-08-256-018-9	Sequence 9, Appl
708	18	36.7	9	2	US-09-865-548A-73	Sequence 73, Appl	781	17	34.7	8	1	US-08-717-169-14	Sequence 14, Appl
709	18	36.7	9	4	PCT-US95-00147-59	Sequence 59, Appl	782	17	34.7	8	1	US-08-762-308-8	Sequence 8, Appl
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711	17	34.7	4	1	US-08-747-137-174	Sequence 174, Ap	784	17	34.7	8	2	US-08-769-745-22	Sequence 22, Appl
712	17	34.7	5	1	US-08-751-767A-77	Sequence 77, Appl	785	17	34.7	8	2	US-08-159-339A-1160	Sequence 1160, Ap
713	17	34.7	5	2	US-09-082-358B-31	Sequence 31, Appl	786	17	34.7	8	2	US-08-444-818-720	Sequence 720, App
714	17	34.7	5	2	US-09-720-041-5	Sequence 5, Appl	787	17	34.7	8	2	US-08-444-818-721	Sequence 721, App
715	17	34.7	5	2	US-10-317-252B-391	Sequence 391, Ap	788	17	34.7	8	2	US-08-444-818-722	Sequence 722, App
716	17	34.7	5	2	US-09-688-017-130	Sequence 130, Ap	789	17	34.7	8	2	US-09-078-173A-20	Sequence 20, Appl
717	17	34.7	6	1	US-08-282-758B-5	Sequence 5, Appl	790	17	34.7	8	2	US-08-706-054A-9	Sequence 9, Appl
718	17	34.7	6	1	US-08-854-222-9	Sequence 9, Appl	791	17	34.7	8	2	US-03-228-901A-14	Sequence 14, Appl
719	17	34.7	6	1	US-08-472-453-58	Sequence 58, Appl	792	17	34.7	8	2	US-09-313-299-9	Sequence 9, Appl
720	17	34.7	6	2	US-09-188-039-9	Sequence 9, Appl	793	17	34.7	8	2	US-09-809-517A-20	Sequence 20, Appl
721	17	34.7	6	2	US-09-455-679-34	Sequence 34, Appl	794	17	34.7	8	4	US-10-042-991-20	Sequence 20, Appl
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723	17	34.7	6	2	US-09-774-639-225	Sequence 225, Ap	796	17	34.7	8	4	PCT-US93-00228-8	Sequence 8, Appl
724	17	34.7	6	2	US-10-317-252B-404	Sequence 404, Ap	797	17	34.7	8	4	PCT-US93-05412-7	Sequence 7, Appl
725	17	34.7	7	1	US-08-472-453-7	Sequence 7, Appl	798	17	34.7	8	4	PCT-US95-04231-8	Sequence 8, Appl
726	17	34.7	7	1	US-08-472-453-37	Sequence 37, Appl	799	17	34.7	9	1	US-08-164-839-62	Sequence 62, Appl
727	17	34.7	7	1	US-08-666-473-17	Sequence 17, Appl	800	17	34.7	9	1	US-08-583-799-62	Sequence 62, Appl
728	17	34.7	7	1	US-08-231-193A-8	Sequence 8, Appl	801	17	34.7	9	1	US-08-102-738-7	Sequence 7, Appl
729	17	34.7	7	1	US-08-893-853-23	Sequence 23, Appl	802	17	34.7	9	1	US-08-102-738-8	Sequence 8, Appl
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733	17	34.7	7	2	US-08-480-474-8	Sequence 8, Appl	806	17	34.7	9	1	US-08-615-181-70	Sequence 70, Appl
734	17	34.7	7	2	US-08-566-190-25	Sequence 25, Appl	807	17	34.7	9	1	US-08-615-181-110	Sequence 110, App
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737	17	34.7	7	2	US-09-352-191-44	Sequence 8, Appl	810	17	34.7	9	1	US-08-340-283-37	Sequence 37, Appl
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739	17	34.7	7	2	US-09-147-933-35	Sequence 35, Appl	812	17	34.7	9	1	US-08-340-283-110	Sequence 110, App
740	17	34.7	7	2	US-09-113-921-23	Sequence 23, Appl	813	17	34.7	9	1	US-08-340-283-123	Sequence 123, App
741	17	34.7	7	2	US-09-078-173A-1	Sequence 1, Appl	814	17	34.7	9	1	US-08-146-028-397	Sequence 397, App
742	17	34.7	7	2	US-09-515-039-11	Sequence 11, Appl	815	17	34.7	9	1	US-08-146-028-440	Sequence 440, App
743	17	34.7	7	2	US-09-352-191-44	Sequence 44, Appl	816	17	34.7	9	1	US-08-934-222-133	Sequence 133, App
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745	17	34.7	7	2	US-08-940-035A-8	Sequence 8, Appl	818	17	34.7	9	1	US-09-207-621-133	Sequence 133, App
746	17	34.7	7	2	US-08-935-105A-8	Sequence 8, Appl	819	17	34.7	9	1	US-08-532-818-133	Sequence 133, App
747	17	34.7	7	2	US-09-447-356-11	Sequence 11, Appl	820	17	34.7	9	2	US-08-159-339A-245	Sequence 245, App
748	17	34.7	7	2	US-09-648-797-8	Sequence 8, Appl	821	17	34.7	9	2	US-08-159-339A-522	Sequence 522, App
749	17	34.7	7	2	US-09-489-847-303	Sequence 303, Ap	822	17	34.7	9	2	US-08-159-339A-1199	Sequence 1199, Ap
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752	17	34.7	7	2	US-09-125-641-13	Sequence 13, Appl	825	17	34.7	9	2	US-08-933-843-133	Sequence 133, App
753	17	34.7	7	2	US-09-520-254-17	Sequence 17, Appl	826	17	34.7	9	2	US-08-934-223-133	Sequence 133, App
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756	17	34.7	7	2	US-09-428-082B-295	Sequence 295, App	829	17	34.7	9	2	US-09-258-754-362	Sequence 362, App
757	17	34.7	7	2	US-09-532-221-50	Sequence 50, Appl	830	17	34.7	9	2	US-09-112-206-397	Sequence 397, App

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833	17	34.7	9	2	US-09-042-107-362	Sequence 362, App	906	16	32.7	5	2	US-09-547-693-216	Sequence 216, App
834	17	34.7	9	2	US-09-413-492-133	Sequence 133, App	907	16	32.7	5	2	US-09-551-976-3	Sequence 3, Appli
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839	17	34.7	9	2	US-09-502-600-133	Sequence 133, App	912	16	32.7	6	1	US-08-079-812-104	Sequence 104, App
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841	17	34.7	9	2	US-08-634-332A-37	Sequence 37, Appl	914	16	32.7	6	1	US-08-505-058-7	Sequence 7, Appli
842	17	34.7	9	2	US-09-311-784A-328	Sequence 328, App	915	16	32.7	6	1	US-08-616-669A-8	Sequence 8, Appli
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846	17	34.7	9	2	US-09-722-250D-362	Sequence 362, App	919	16	32.7	6	2	US-08-482-085B-4	Sequence 4, Appli
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848	17	34.7	9	2	US-09-918-243-133	Sequence 133, App	921	16	32.7	6	2	US-08-246-441-15	Sequence 15, Appl
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851	17	34.7	9	2	US-09-454-204A-45	Sequence 45, Appl	924	16	32.7	6	2	US-09-326-440-39	Sequence 39, Appl
852	17	34.7	9	2	US-09-576-824A-388	Sequence 388, App	925	16	32.7	6	2	US-09-326-440-41	Sequence 41, Appl
853	17	34.7	9	2	US-09-647-372B-59	Sequence 59, Appl	926	16	32.7	6	2	US-09-232-446B-3	Sequence 3, Appli
854	17	34.7	9	2	US-09-601-729-244	Sequence 244, App	927	16	32.7	6	2	US-09-232-446B-20	Sequence 20, Appl
855	17	34.7	9	2	US-09-192-854-98	Sequence 98, Appl	928	16	32.7	6	2	US-09-230-944-7	Sequence 7, Appli
856	17	34.7	9	2	US-09-920-174-12	Sequence 12, Appl	929	16	32.7	6	2	US-09-343-011B-5	Sequence 5, Appli
857	17	34.7	9	2	US-09-920-174-12	Sequence 12, Appl	930	16	32.7	6	2	US-09-444-791A-4	Sequence 4, Appli
858	17	34.7	9	2	US-09-680-497-397	Sequence 397, App	931	16	32.7	6	2	US-09-636-252A-16	Sequence 16, Appl
859	17	34.7	9	2	US-09-680-497-440	Sequence 440, App	932	16	32.7	6	2	US-09-393-585-15	Sequence 15, Appl
860	17	34.7	9	2	US-09-281-760B-17	Sequence 17, Appl	933	16	32.7	6	2	US-09-873-233A-7	Sequence 7, Appli
861	17	34.7	9	2	US-09-281-760B-24	Sequence 24, Appl	934	16	32.7	6	2	US-09-458-631-6	Sequence 6, Appli
862	17	34.7	9	2	US-09-676-475A-362	Sequence 362, App	935	16	32.7	6	2	US-09-458-631B-29	Sequence 29, Appl
863	17	34.7	9	2	US-09-631-863A-67	Sequence 67, Appl	936	16	32.7	6	2	US-09-454-651B-32	Sequence 32, Appl
864	17	34.7	9	2	US-09-631-863A-88	Sequence 88, Appl	937	16	32.7	6	2	US-09-454-651B-28	Sequence 28, Appl
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866	17	34.7	9	2	US-09-511-939-174	Sequence 174, App	939	16	32.7	6	2	PCT-US93-07306-48	Sequence 48, Appl
867	17	34.7	9	2	US-09-865-548A-82	Sequence 82, Appl	940	16	32.7	6	4	PCT-US93-07306-48	Sequence 48, Appl
868	17	34.7	9	2	US-10-607-595-362	Sequence 362, App	941	16	32.7	7	1	US-07-956-848A-37	Sequence 37, Appl
869	17	34.7	9	2	US-09-977-831-4	Sequence 4, Appli	942	16	32.7	7	1	US-08-137-499A-32	Sequence 32, Appl
870	17	34.7	9	4	PCT-US92-07865-5	Sequence 5, Appli	943	16	32.7	7	1	US-08-137-499A-34	Sequence 34, Appl
871	17	34.7	9	4	PCT-US94-01840-12	Sequence 12, Appl	944	16	32.7	7	1	US-08-482-847-32	Sequence 32, Appl
872	17	34.7	9	4	PCT-US94-14106-36	Sequence 36, Appl	945	16	32.7	7	1	US-08-482-847-34	Sequence 34, Appl
873	17	34.7	9	6	5395760-12	Patent No. 5395760	946	16	32.7	7	1	US-08-218-027A-4	Sequence 4, Appli
874	16	32.7	4	1	US-08-048-164A-13	Sequence 13, Appl	947	16	32.7	7	1	US-08-218-027A-5	Sequence 5, Appli
875	16	32.7	4	1	US-08-358-160-174	Sequence 174, App	948	16	32.7	7	1	US-08-218-027A-7	Sequence 7, Appli
876	16	32.7	4	1	US-08-451-240-1	Sequence 1, Appli	949	16	32.7	7	1	US-08-471-956-37	Sequence 37, Appl
877	16	32.7	4	1	US-08-460-462-13	Sequence 13, Appl	950	16	32.7	7	1	US-08-666-473-18	Sequence 18, Appl
878	16	32.7	4	1	US-08-460-457-13	Sequence 13, Appl	951	16	32.7	7	1	US-08-666-473-20	Sequence 20, Appl
879	16	32.7	4	1	US-08-460-458-13	Sequence 13, Appl	952	16	32.7	7	1	US-08-666-473-21	Sequence 21, Appl
880	16	32.7	4	1	US-08-737-927-5	Sequence 5, Appli	953	16	32.7	7	1	US-08-632-598-34	Sequence 34, Appl
881	16	32.7	4	1	US-08-776-665-1	Sequence 1, Appli	954	16	32.7	7	1	US-08-350-260A-421	Sequence 421, App
882	16	32.7	4	1	US-08-460-455-13	Sequence 13, Appl	955	16	32.7	7	1	US-08-449-645A-1	Sequence 1, Appli
883	16	32.7	4	1	US-08-470-846A-1	Sequence 1, Appli	956	16	32.7	7	1	US-08-702-367A-1	Sequence 1, Appli
884	16	32.7	4	1	US-08-330-394A-13	Sequence 13, Appl	957	16	32.7	7	2	US-08-930-503A-8	Sequence 8, Appli
885	16	32.7	4	2	US-09-954-915A-30	Sequence 30, Appl	958	16	32.7	7	2	US-09-193-365-119	Sequence 119, App
886	16	32.7	4	2	US-09-154-390-1	Sequence 1, Appli	959	16	32.7	7	2	US-09-231-240-34	Sequence 34, Appl
887	16	32.7	4	4	PCT-US94-12591-1	Sequence 1, Appli	960	16	32.7	7	2	US-09-085-072-2	Sequence 2, Appli
888	16	32.7	5	1	US-08-014-979-54	Sequence 54, Appl	961	16	32.7	7	2	US-09-084-605B-24	Sequence 24, Appl
889	16	32.7	5	1	US-08-477-509B-9	Sequence 9, Appli	962	16	32.7	7	2	US-09-104-337A-421	Sequence 421, App
890	16	32.7	5	1	US-08-177-109A-56	Sequence 56, Appl	963	16	32.7	7	2	US-09-007-288B-155	Sequence 155, App
891	16	32.7	5	1	US-08-687-706-56	Sequence 56, Appl	964	16	32.7	7	2	US-09-437-136-4	Sequence 4, Appli
892	16	32.7	5	2	US-08-482-085B-9	Sequence 9, Appli	965	16	32.7	7	2	US-09-437-136-5	Sequence 5, Appli
893	16	32.7	5	2	US-08-649-100-19	Sequence 19, Appl	966	16	32.7	7	2	US-10-394-980-124	Sequence 124, App
894	16	32.7	5	2	US-08-649-100-35	Sequence 35, Appl	967	16	32.7	7	2	US-10-655-201-4	Sequence 4, Appli
895	16	32.7	5	2	US-08-976-255-50	Sequence 50, Appl	968	16	32.7	7	2	US-10-655-201-5	Sequence 5, Appli
896	16	32.7	5	2	US-08-591-632-25	Sequence 25, Appl	969	16	32.7	7	4	PCT-US95-04681-1	Sequence 1, Appli
897	16	32.7	5	2	US-09-296-089-3	Sequence 3, Appli	970	16	32.7	8	1	US-08-036-555B-45	Sequence 45, Appl
898	16	32.7	5	2	US-09-444-791A-9	Sequence 9, Appli	971	16	32.7	8	1	US-08-469-569-45	Sequence 45, Appl
899	16	32.7	5	2	US-09-099-053-4	Sequence 4, Appli	972	16	32.7	8	1	US-08-382-013A-43	Sequence 43, Appl
900	16	32.7	5	2	US-09-611-451-25	Sequence 25, Appl	973	16	32.7	8	1	US-08-321-625-89	Sequence 89, Appl
901	16	32.7	5	2	US-09-119-507B-3	Sequence 3, Appli	974	16	32.7	8	1	US-08-249-322A-45	Sequence 45, Appl
902	16	32.7	5	2	US-08-897-556A-3	Sequence 3, Appli	975	16	32.7	8	1	US-08-462-894-23	Sequence 23, Appl
903	16	32.7	5	2	US-08-897-556A-105	Sequence 105, App	976	16	32.7	8	1	US-08-189-331-151	Sequence 151, App

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981 16 32.7 8 1 US-08-734-591A-45
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985 16 32.7 8 2 US-08-341-018-78
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987 16 32.7 8 2 US-08-863-813A-20
988 16 32.7 8 2 US-08-470-335-45
989 16 32.7 8 2 US-09-181-083-89
990 16 32.7 8 2 US-08-735-021-45
991 16 32.7 8 2 US-08-734-664A-45
992 16 32.7 8 2 US-08-470-339-45
993 16 32.7 8 2 US-08-676-318A-19
994 16 32.7 8 2 US-08-676-318A-20
995 16 32.7 8 2 US-09-296-089-10
996 16 32.7 8 2 US-09-296-089-11
997 16 32.7 8 2 US-09-296-089-12
998 16 32.7 8 2 US-09-296-089-13
999 16 32.7 8 2 US-09-296-089-22
1000 16 32.7 8 2 US-09-561-500-38

ALIGNMENTS

RESULT 1
US-08-787-547-55
; Sequence 55, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-787-547-55
Query Match 79.6%; Score 39; DB 1; Length 9;
Best Local Similarity 77.8%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 STAPPVHNV 9
DB 1 STAPPAHGV 9
RESULT 2
US-08-288-059-19
; Sequence 19, Application US/08288059
; Patent No. 5827866
; GENERAL INFORMATION:
; APPLICANT: FINN, OLIVERA J.
; APPLICANT: FONTENOT, J. D.
; APPLICANT: MONTELARO, RONALD C.
; TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN
; TITLE OF INVENTION: AND MUCIN-LIKE PEPTIDES, AND USES THEREOF
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,059
; FILING DATE: 08-AUG-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAPIN, MARLANA K.
; REGISTRATION NUMBER: 35,843
; REFERENCE/DOCKET NUMBER: 61137/205204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-288-059-19
Query Match 79.6%; Score 39; DB 1; Length 9;
Best Local Similarity 77.8%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 STAPPVHNV 9
DB 1 STAPPAHGV 9
RESULT 3
US-09-593-870A-45
; Sequence 45, Application US/09593870A
; Patent No. 6548643
; GENERAL INFORMATION:
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Apostolopoulos, Vasso
; APPLICANT: Pietersz, Geoff Allan
; TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their

;; TITLE OF INVENTION: Use in Immunotherapy
;; FILE REFERENCE: 2368-McKenzie
;; CURRENT APPLICATION NUMBER: US/09/593,870A
;; CURRENT FILING DATE: 2000-06-14
;; PRIOR APPLICATION NUMBER: 09/223,043
;; PRIOR FILING DATE: 1998-12-30
;; NUMBER OF SEQ ID NOS: 69
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 45
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-593-870A-45

Query Match 79.6%; Score 39; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STAPPVHV 9
| | | | | | |
Db 1 STAPPAGV 9

RESULT 4
US-09-497-232-1
; Sequence 1, Application US/09497232
; Patent No. 6600012
; GENERAL INFORMATION:
; APPLICANT: AGRAWAL, Babita
; KRANTZ, Mark J.
; REDDISH, Mark A.
; LONGENECKER, B. Michael
; TITLE OF INVENTION: METHOD FOR GENERATING ACTIVATED T-CELLS
; AND ANTIGEN-PULSED ANTIGEN-PRESENTING CELLS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/497,232
; FILING DATE: 03-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,410
; FILING DATE: 08-MAY-1998
; APPLICATION NUMBER: US 60/045,949
; FILING DATE: 08-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 042881/0114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-497-232-1

Query Match 79.6%; Score 39; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STAPPVHV 9
| | | | | | |
Db 1 STAPPAGV 9

RESULT 5
US-10-296-317-44
; Sequence 44, Application US/10296317
; Patent No. 6951647
; GENERAL INFORMATION:
; APPLICANT: CEL-Sci Corp
; APPLICANT: Zimmermann, Daniel S
; APPLICANT: Sarin, Prem S
; TITLE OF INVENTION: T CELL BINDING LIGAND PEPTIDES, PEPTIDE
; FILE REFERENCE: CS-112
; CURRENT APPLICATION NUMBER: US/10/296,317
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/206548
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: PCT/US07/16793
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Muc1 Peptide M1b
US-10-296-317-44

Query Match 79.6%; Score 39; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STAPPVHV 9
| | | | | | |
Db 1 STAPPAGV 9

RESULT 6
US-09-497-232-25
; Sequence 25, Application US/09497232
; Patent No. 6600012
; GENERAL INFORMATION:
; APPLICANT: AGRAWAL, Babita
; KRANTZ, Mark J.
; REDDISH, Mark A.
; LONGENECKER, B. Michael
; TITLE OF INVENTION: METHOD FOR GENERATING ACTIVATED T-CELLS
; AND ANTIGEN-PULSED ANTIGEN-PRESENTING CELLS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/497,232
; FILING DATE: 03-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,410
; FILING DATE: 08-MAY-1998
; APPLICATION NUMBER: US 60/045,949
; FILING DATE: 08-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 042881/0114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-497-232-1

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; APPLICATION NUMBER: US/09/074,410
; FILING DATE: 08-MAY-1998
; APPLICATION NUMBER: US 60/045,949
; FILING DATE: 08-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 042881/0114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-497-232-25

Query Match      73.5%; Score 36; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 STAPPVHV 9
      :|||||
Db      1 ATAPPAGV 9

RESULT 7
US-08-288-059-17
; Sequence 17, Application US/08288059
; Patent No. 5827666
; GENERAL INFORMATION:
; APPLICANT: FINN, OLIVERA J.
; APPLICANT: FONTELOT, J. D.
; APPLICANT: MONTELLARO, RONALD C.
; TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,059
; FILING DATE: 08-AUG-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAPIN, MARLANA K.
; REGISTRATION NUMBER: 35,843
; REFERENCE/DOCKET NUMBER: 61137/205204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-288-059-17
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Query Match      71.4%; Score 35; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 STAPPVH 7
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Db      3 STAPPAH 9

RESULT 8
US-08-288-059-18
; Sequence 18, Application US/08288059
; Patent No. 5827666
; GENERAL INFORMATION:
; APPLICANT: FINN, OLIVERA J.
; APPLICANT: FONTELOT, J. D.
; APPLICANT: MONTELLARO, RONALD C.
; TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,059
; FILING DATE: 08-AUG-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAPIN, MARLANA K.
; REGISTRATION NUMBER: 35,843
; REFERENCE/DOCKET NUMBER: 61137/205204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-288-059-18

Query Match      71.4%; Score 35; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 STAPPVH 7
      :|||||
Db      2 STAPPAH 8

RESULT 9
US-08-288-059-20
; Sequence 20, Application US/08288059
; Patent No. 5827666
; GENERAL INFORMATION:
; APPLICANT: FINN, OLIVERA J.
; APPLICANT: FONTELOT, J. D.
; APPLICANT: MONTELLARO, RONALD C.
; TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,059
; FILING DATE: 08-AUG-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAPIN, MARLANA K.
; REGISTRATION NUMBER: 35,843
; REFERENCE/DOCKET NUMBER: 61137/205204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-288-059-17
```

NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288.059
FILING DATE: 08-AUG-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CHAPIN, MARLANA K.
REGISTRATION NUMBER: 35,843
REFERENCE/DOCKET NUMBER: 61137/205204
TELEPHONE: 202-861-3711
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-288-059-20

Query Match 71.4%; Score 35; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TAPPVHV 9
| | | | |
Db 1 TAPPAGV 8

RESULT 10
US-09-593-870A-68
Sequence 68, Application US/09593870A
Patent No. 6548643
GENERAL INFORMATION:
APPLICANT: McKenzie, Ian F.C.
APPLICANT: Apostolopoulos, Vasso
APPLICANT: Pieterse, Geoff Allan
TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
TITLE OF INVENTION: Use in Immunotherapy
FILE REFERENCE: 2368-McKenzie
CURRENT APPLICATION NUMBER: US/09/593.870A
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 09/223,043
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 68
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-593-870A-68

Query Match 71.4%; Score 35; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TAPPVHV 9
| | | | |
Db 1 TAPPAGV 8

RESULT 11
US-08-134-198E-23
Sequence 23, Application US/08134198E
Patent No. 6190885
GENERAL INFORMATION:
APPLICANT: CANCER RESEARCH FUND
APPLICANT: OF CONTRA COSTA
APPLICANT: PETERSON, JERRY A.
APPLICANT: LAROCCA, DAVID J.
TITLE OF INVENTION: FUSION PROTEIN CONTAINING HMFG
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower Street, Suite 1900
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134.198E
FILING DATE: October 8, 1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38208 (CRFC-003C)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-134-198E-23

Query Match 63.3%; Score 31; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TAPPVH 7
| | | | |
Db 1 TAPPAG 6

RESULT 12
US-08-288-059-21
Sequence 21, Application US/08288059
Patent No. 5827666
GENERAL INFORMATION:
APPLICANT: FINN, OLIVERA J.
APPLICANT: FONTENOT, J. D.
APPLICANT: MONTECARO, RONALD C.
TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN
TITLE OF INVENTION: AND MUCIN-LIKE PEPTIDES, AND USES THEREOF
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,059
; FILING DATE: 08-AUG-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAPIN, MARLANA K.
; REGISTRATION NUMBER: 35,843
; REFERENCE/DOCKET NUMBER: 61137/205204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-288-059-21

Query Match 61.2%; Score 30; DB 1; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 APPVHNV 9
Db 1 APPAHGV 7

RESULT 13
US-09-593-870A-67
; Sequence 67, Application US/09593870A
; Patent No. 6548643
; GENERAL INFORMATION:
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Apostolopoulos, Vasso
; APPLICANT: Pietercz, Geoff Allan
; TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
; FILE REFERENCE: Use in Immunotherapy
; CURRENT APPLICATION NUMBER: US/09/593,870A
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/223,043
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; APPLICANT: CANCER RESEARCH FUND
US-09-593-870A-67

Query Match 61.2%; Score 30; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 APPVHNV 9
Db 1 APPAHGV 7

RESULT 14
US-08-134-198E-21
; Sequence 21, Application US/08134198E
; Patent No. 6190885
; GENERAL INFORMATION:
; APPLICANT: CANCER RESEARCH FUND
```

```
; APPLICANT: OF CONTRA COSTA
; APPLICANT: PETERSON, JERRY A.
; APPLICANT: LAROCCA, DAVID J.
; TITLE OF INVENTION: FUSION PROTEIN CONTAINING HMFG
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower Street, Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,198E
; FILING DATE: October 8, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38208 (CRFC-003C)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-134-198E-21

Query Match 55.1%; Score 27; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPP 5
Db 2 STAPP 6

RESULT 15
US-08-134-198E-22
; Sequence 22, Application US/08134198E
; Patent No. 6190885
; GENERAL INFORMATION:
; APPLICANT: CANCER RESEARCH FUND
; APPLICANT: OF CONTRA COSTA
; APPLICANT: PETERSON, JERRY A.
; APPLICANT: LAROCCA, DAVID J.
; TITLE OF INVENTION: FUSION PROTEIN CONTAINING HMFG
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower Street, Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,198E
```


; FILING DATE: October 8, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38208 (CRFC-003C)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-134-198E-22

Query Match 55.1%; Score 27; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPP 5
Db 1 STAPP 5
|||||

RESULT 16
US-08-288-059-16
; Sequence 16, Application US/08288059
; Patent No. 5827866
; GENERAL INFORMATION:
; APPLICANT: FINN, OLIVERA J.
; APPLICANT: FONTENOT, J. D.
; APPLICANT: MONTELAPO, RONALD C.
; TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN, L.L.P.
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,059
; FILING DATE: 08-AUG-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CHAPIN, MARLANA K.
; REGISTRATION NUMBER: 35,843
; REFERENCE/DOCKET NUMBER: 61137/205204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-288-059-16

Query Match 55.1%; Score 27; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPP 5
Db 4 STAPP 8
|||||

RESULT 17
US-09-593-870A-43
; Sequence 43, Application US/09593870A
; Patent No. 6548643
; GENERAL INFORMATION:
; APPLICANT: Mckenzie, Ian F.C.
; APPLICANT: Apostolopoulos, Vasso
; APPLICANT: Pietersz, Geoff Allan
; TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
; TITLE OF INVENTION: Use in Immunotherapy
; FILE REFERENCE: 2368-Mckenzie
; CURRENT APPLICATION NUMBER: US/09/593,870A
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/223,043
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-593-870A-43

Query Match 55.1%; Score 27; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPP 5
Db 4 STAPP 8
|||||

RESULT 18
US-08-134-198E-24
; Sequence 24, Application US/08134198E
; Patent No. 6190885
; GENERAL INFORMATION:
; APPLICANT: CANCER RESEARCH FUND
; APPLICANT: OF CONTRA COSTA
; APPLICANT: PETERSON, JERRY A.
; APPLICANT: LAROCCA, DAVID J.
; TITLE OF INVENTION: FUSION PROTEIN CONTAINING HMFG
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower Street, Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,198E
; FILING DATE: October 8, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38208 (CRFC-003C)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700

```
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-134-198E-24

Query Match 53.1%; Score 26; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPVHV 7
DB 1 APPAH 5

RESULT 19
US-08-134-198E-25
; Sequence 25, Application US/08134198E
; Patent No. 6190885
; GENERAL INFORMATION:
; APPLICANT: CANCER RESEARCH FUND
; APPLICANT: OF CONTRA COSTA
; APPLICANT: PETERSON, JERRY A.
; APPLICANT: LAROCCA, DAVID J.
; TITLE OF INVENTION: FUSION PROTEIN CONTAINING HMFG
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower Street, Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,198E
; FILING DATE: October 8, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38208 (CRFC-003C)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-134-198E-25

Query Match 53.1%; Score 26; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPVHV 9
DB 1 PPAHV 6

RESULT 20
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-134-198E-24

Query Match 53.1%; Score 26; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PPVHV 7
DB 1 APPAH 5

RESULT 19
US-08-134-198E-25
; Sequence 25, Application US/08134198E
; Patent No. 6190885
; GENERAL INFORMATION:
; APPLICANT: CANCER RESEARCH FUND
; APPLICANT: OF CONTRA COSTA
; APPLICANT: PETERSON, JERRY A.
; APPLICANT: LAROCCA, DAVID J.
; TITLE OF INVENTION: FUSION PROTEIN CONTAINING HMFG
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower Street, Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,198E
; FILING DATE: October 8, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38208 (CRFC-003C)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-134-198E-25

Query Match 53.1%; Score 26; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPVHV 9
DB 1 PPAHV 6

RESULT 20
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-134-198E-24

Query Match 53.1%; Score 26; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPVH 7
DB 4 PPVH 7

RESULT 21
US-08-288-059-22
; Sequence 22, Application US/08288059
; Patent No. 5827666
; GENERAL INFORMATION:
; APPLICANT: FINN, OLIVERA J.
; APPLICANT: FONTENOT, J. D.
; APPLICANT: MONTELARO, RONALD C.
; TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN
; TITLE OF INVENTION: AND MUCIN-LIKE PEPTIDES, AND USES THEREOF
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; US-08-472-453-4
; Sequence 4, Application US/08472453
; Patent No. 5831002
; GENERAL INFORMATION:
; APPLICANT: Haupt, Andreas
; APPLICANT: Emling, Franz
; APPLICANT: Romerdahl, Cynthia
; TITLE OF INVENTION: No. 5831002el Compounds, The Preparation and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patricia Granahan, Esq., Hamilton, Brook, Smith &
; ADDRESSEE: Reynolds, P.C.
; STREET: Two Milita Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,453
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/431,795
; FILING DATE: 05-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,696
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/885,788
; FILING DATE: 20-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia.
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: BHC-029C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781 8616240
; TELEFAX: 781 8619540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-472-453-4

Query Match 53.1%; Score 26; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPVH 7
DB 4 PPVH 7
```

ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,059
FILING DATE: 08-AUG-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CHAPIN, MARLANA K.
REGISTRATION NUMBER: 35,843
REFERENCE/DOCKET NUMBER: 61137/205204
TELEPHONE: 202-861-3711
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-288-059-22

Query Match 53.1%; Score 26; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0;

Qy 4 PPVHNV 9
Db 1 PPAHGV 6

RESULT 22
US-08-210-266A-1
; Sequence 1, Application US/08210266A
; Patent No. 5545619
; GENERAL INFORMATION:
; APPLICANT: Atkinson, John P.
; APPLICANT: Hourcade, Dennis
; APPLICANT: Krych, Malgorzata
; TITLE OF INVENTION: Modified Complement System
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/210,266A
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,514
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note="K/R"
FEATURE:
NAME/KEY: Modified-site

REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-210-266A-1

Query Match 51.0%; Score 25; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0;

Qy 1 STAPPV 6
Db 1 STKPP1 6

RESULT 23
US-08-210-266A-8
; Sequence 8, Application US/08210266A
; Patent No. 5545619
; GENERAL INFORMATION:
; APPLICANT: Atkinson, John P.
; APPLICANT: Hourcade, Dennis
; APPLICANT: Krych, Malgorzata
; TITLE OF INVENTION: Modified Complement System
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/210,266A
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,514
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note="K/R"
FEATURE:
NAME/KEY: Modified-site

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; ; LOCATION: 6
; ; OTHER INFORMATION: /note= "I/L/V"
; ; FEATURE:
; ; NAME/KEY: Modified-site
; ; LOCATION: 8
; ; OTHER INFORMATION: /note= "Q/N"
US-08-210-266A-8

Query Match 51.0%; Score 25; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STAPPV 6
Db 1 STKPPI 6

RESULT 24
US-08-688-675-1
; Sequence 1, Application US/08688675
; Patent No. 5719127
; GENERAL INFORMATION:
; APPLICANT: Atkinson, John P.
; APPLICANT: Hourcade, Dennis
; APPLICANT: Krych, Malgorzata
; TITLE OF INVENTION: Modified Complement System Regulators
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,675
; FILING DATE: 30-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/210,266
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/695,514
; FILING DATE: 03-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU101div2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)873-8794
; TELEFAX: (404)873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "K/R"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "I/L/V"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note= "Q/N"
US-08-688-675-8

Query Match 51.0%; Score 25; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STAPPV 6
Db 1 STKPPI 6

RESULT 25
US-08-688-675-8
; Sequence 8, Application US/08688675
; Patent No. 5719127
; GENERAL INFORMATION:
; APPLICANT: Atkinson, John P.
; APPLICANT: Hourcade, Dennis
; APPLICANT: Krych, Malgorzata
; TITLE OF INVENTION: Modified Complement System Regulators
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1201 West Peachtree
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,675
; FILING DATE: 30-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/210,266
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/695,514
; FILING DATE: 03-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU101div2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)873-8794
; TELEFAX: (404)873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "K/R"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "I/L/V"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note= "Q/N"
US-08-688-675-8

Query Match 51.0%; Score 25; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STAPPV 6
Db 1 STKPPI 6

RESULT 26
US-08-477-860C-1
; Sequence 1, Application US/08477860C
```

Patent No. 6010873
GENERAL INFORMATION:
APPLICANT: Atkinson, John P.
APPLICANT: Hourcade, Dennis
APPLICANT: Kiyoh, Malgorzata
TITLE OF INVENTION: Modified Complement System Regulators
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree
CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,860C
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/210,266
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,514
FILING DATE: 03-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 101 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-860C-1

Query Match 51.0%; Score 25; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STAPPV 6
Db 1 STKPI 6

RESULT 27
US-100-930A-22
Sequence 22, Application US/09100930A
Patent No. 6248549
GENERAL INFORMATION:
APPLICANT: Van Eyk, Jennifer E.
APPLICANT: Mak, Alan S.
APPLICANT: Cote, Graham P.
TITLE OF INVENTION: Methods of Modulating Muscle Contraction
FILE REFERENCE: 1997-021-03US
CURRENT APPLICATION NUMBER: US/09/100,930A
CURRENT FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/050,478
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 60/089,505
PRIOR FILING DATE: 1998-06-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22

LENGTH: 9
TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(9)
OTHER INFORMATION: PAK site A autophosphorylation
NAME/KEY: PEPTIDE
LOCATION: (9)
OTHER INFORMATION: Targeted Ser phospho-amino acid
US-09-100-930A-22

Query Match 51.0%; Score 25; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 APPVHN 8
Db 2 APPMRN 7

RESULT 28
US-08-403-459-67
Sequence 67, Application US/08403459
Patent No. 6514942
GENERAL INFORMATION:
APPLICANT: Ioannides, Constantin G.
APPLICANT: Fisk, Bryan A.
APPLICANT: Ioannides, Maria G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
TITLE OF INVENTION: T-LYMPHOCYTES
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,459
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSC:390/KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-403-459-67

Query Match 51.0%; Score 25; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 STAPPVHN 9
Db 1 SLADPAHGV 9

```

; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16887/837
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-666-473-24

Query Match 49.0%; Score 24; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STAPP 5
Db :|||
3 ATAPP 7

RESULT 31
US-08-444-818-340
; Sequence 340, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 340:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-444-818-340

Query Match 49.0%; Score 24; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 STAPPVHN 8
:|||||

```

Db 1 NTRPPLGN 8

RESULT 32

US-08-338-634-16

; Sequence 16, Application US/08338634

; Patent No. 5679641

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Peptides of human p53 protein for use

; TITLE OF INVENTION: in human T cell response inducing compositions, and

; TITLE OF INVENTION: human p53 protein-specific cytotoxic T-lymphocytes.

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hoffmann & Baron

; STREET: 350 Jericho Turnpike

; CITY: Jericho

; STATE: New York

; COUNTRY: United States of America

; ZIP: 11758

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/338,634

; FILING DATE: 06-February-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/NL93/00102

; FILING DATE: 18-May-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Baron, Ronald J.

; REGISTRATION NUMBER: 29,281

; REFERENCE/DOCKET NUMBER: 294-26

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 822-3550

; TELEFAX: (516) 822-3582

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

US-08-338-634-16

Query Match 49.0%; Score 24; DB 1; Length 9;

Best Local Similarity 80.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 APPVH 7

Db 3 APPQH 7

RESULT 33

US-09-601-729-98

; Sequence 98, Application US/09601729

; Patent No. 6683052

; GENERAL INFORMATION:

; APPLICANT: THIAM, KADER

; APPLICANT: AURIAULT, CLAUDE

; APPLICANT: GRAS-MASSE, HELENE

; APPLICANT: LOING, ESTELLE

; APPLICANT: VERWAERDE, CLAUDIE

; APPLICANT: GUILLET, JEAN GERARD

; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES

; FILE REFERENCE: USB-97-AU-IN

; CURRENT APPLICATION NUMBER: US/09/601,729

; FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: PCT/FR99/00259

; PRIOR FILING DATE: 1999-02-05

; PRIOR APPLICATION NUMBER: 98 01439

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 281

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 98

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-601-729-102

Query Match 49.0%; Score 24; DB 2; Length 9;

Best Local Similarity 80.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 APPVH 7

Db 3 APPQH 7

RESULT 34

US-09-601-729-102

; Sequence 102, Application US/09601729

; Patent No. 6683052

; GENERAL INFORMATION:

; APPLICANT: THIAM, KADER

; APPLICANT: AURIAULT, CLAUDE

; APPLICANT: GRAS-MASSE, HELENE

; APPLICANT: LOING, ESTELLE

; APPLICANT: VERWAERDE, CLAUDIE

; APPLICANT: GUILLET, JEAN GERARD

; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES

; FILE REFERENCE: USB-97-AU-IN

; CURRENT APPLICATION NUMBER: US/09/601,729

; FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: PCT/FR99/00259

; PRIOR FILING DATE: 1999-02-05

; PRIOR APPLICATION NUMBER: 98 01439

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 281

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 102

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-601-729-102

Query Match 49.0%; Score 24; DB 2; Length 9;

Best Local Similarity 80.0%; Pred. No. 4.6e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 APPVH 7

Db 3 APPQH 7

RESULT 35

US-08-188-228-1

; Sequence 1, Application US/08188228

; Patent No. 5597725

; GENERAL INFORMATION:

; APPLICANT: Suzuki, Shintaro

; TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS

; NUMBER OF SEQUENCES: 62

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-188-228-1

Query Match 46.9%; Score 23; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 TAPP 5
Db 1 TAPP 4

RESULT 36
US-08-332-643-1
Sequence 1, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-332-643-1

Query Match 46.9%; Score 23; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 TAPP 5
Db 1 TAPP 4

RESULT 37
US-08-332-638-1
Sequence 1, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-332-638-1

Query Match 46.9%; Score 23; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAPP 5
|:|
DB 1 TAPP 4

RESULT 38
US-09-005-215-29
; Sequence 29, Application US/09005215
; Patent No. 6172043
; GENERAL INFORMATION:
; APPLICANT: Ingram, Vernon M.
; APPLICANT: Blanchard, Barbara J.
; TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S
; TITLE OF INVENTION: DISEASE CAUSED BY -AMYLOID PEPTIDES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,215
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/035,847
; FILING DATE: 10-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/960,188
; FILING DATE: 29-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Gates, Edward R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: M0656/7035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO

Query Match 46.9%; Score 23; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STAPP 5
|:|
DB 1 SSAPP 5

RESULT 39
US-09-706-574A-29
; Sequence 29, Application US/09706574A
; Patent No. 6942963
; GENERAL INFORMATION:

; APPLICANT: Ingram, Vernon M.
; APPLICANT: Blanchard, Barbara J.
; TITLE OF INVENTION: TREATMENTS FOR NEUROTOXICITY IN ALZHEIMER'S DISEASE CAUSED BY
; TITLE OF INVENTION: a-AMYLOID PEPTIDES
; FILE REFERENCE: M0656/7060
; CURRENT APPLICATION NUMBER: US/09/706,574A
; CURRENT FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/035,847
; PRIOR FILING DATE: 1997-01-10
; PRIOR APPLICATION NUMBER: US 08/960,188
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: US 09/005,215
; PRIOR FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-706-574A-29

Query Match 46.9%; Score 23; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STAPP 5
|:|
DB 1 SSAPP 5

RESULT 40
US-09-192-854-91
; Sequence 91, Application US/09192854
; Patent No. 6696245
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 91
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-91

Query Match 46.9%; Score 23; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAPP 5
|:|
DB 1 TAPP 4

RESULT 41
US-09-511-939-159
; Sequence 159, Application US/09511939
; Patent No. 6846634
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1070
; CURRENT APPLICATION NUMBER: US/09/511,939
; CURRENT FILING DATE: 2002-04-10

```
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 159
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-511-939-159

Query Match          46.9%; Score 23; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAPP 5
   ||||
DB 1 TAPP 4

RESULT 42
US-08-615-181-21
; Sequence 21, Application US/08615181
; Patent No. 5756666
; GENERAL INFORMATION:
; APPLICANT: MASAFUMI, TAKIGUCHI
; APPLICANT: MIWA, KIYOSHI
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,181
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01756
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 261302/1993
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-796-0 PCT
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; ORIGINAL SOURCE:
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; US-08-615-181-81

Query Match          46.9%; Score 23; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PVHNV 9
   ||||
DB 2 PVHGV 6

; ORIGINAL SOURCE:
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; US-08-615-181-21

Query Match          46.9%; Score 23; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PVHNV 9
   ||||
DB 2 PVHGV 6
```

RESULT 44

US-08-477-860C-8
 ; Sequence 8, Application US/08477860C
 ; Patent No. 6010873
 ; GENERAL INFORMATION:
 ; APPLICANT: Atkinson, John P.
 ; APPLICANT: Hourcade, Dennis
 ; APPLICANT: Krych, Malgorzata
 ; TITLE OF INVENTION: Modified Complement System Regulators
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patrea L. Pabst
 ; STREET: 2800 One Atlantic Center, 1201 West Peachtree
 ; STREET: Street
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: US
 ; ZIP: 30309-3450
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,860C
 ; FILING DATE: 7-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/210,266
 ; FILING DATE: 18-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/695,514
 ; FILING DATE: 03-MAY-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pabst, Patrea L.
 ; REGISTRATION NUMBER: 31,284
 ; REFERENCE/DOCKET NUMBER: WU 101 DIV
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (404)873-8794
 ; TELEFAX: (404)873-8795
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 3
 ; OTHER INFORMATION: /note= Xaa can be Lys or Arg
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 6
 ; OTHER INFORMATION: /note= Xaa can be Ile, Leu, or Val
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 8
 ; OTHER INFORMATION: /note= Xaa can be Gln or Asn
 ; US-08-477-860C-8

Query Match 46.9%; Score 23; DB 2; Length 8;
 Best Local Similarity 80.0%; Pred. No. 4.6e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STAPP 5
 Db 1 STXPP 5

RESULT 45

US-08-444-818-341
 ; Sequence 341, Application US/08444818

; Patent No. 6150087
 ; GENERAL INFORMATION:
 ; APPLICANT: Chien, David Y.
 ; APPLICANT: Rutter, William J.
 ; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
 ; NUMBER OF SEQUENCES: 777
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: 4560 Horton Street
 ; CITY: Emeryville
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94608-2916
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/444,818
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/403,590
 ; FILING DATE: 14-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Harbin, Alisa A.
 ; REGISTRATION NUMBER: 33,895
 ; REFERENCE/DOCKET NUMBER: 0110.002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (508)359-3876
 ; TELEFAX: (508)359-3885
 ; INFORMATION FOR SEQ ID NO: 341:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-444-818-341

Query Match 46.9%; Score 23; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 4.6e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TAPPVHN 8
 Db 1 TRPPLGN 7

RESULT 46

US-10-185-815A-76
 ; Sequence 76, Application US/10185815A
 ; Patent No. 6916789
 ; GENERAL INFORMATION:
 ; APPLICANT: Elan Corporation, plc
 ; APPLICANT: O'Mahony, Daniel
 ; APPLICANT: Lambkin, Imelda
 ; APPLICANT: Higgins, Lisa
 ; TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands
 ; FILE REFERENCE: P26,480-A USA
 ; CURRENT APPLICATION NUMBER: US/10/185,815A
 ; CURRENT FILING DATE: 2002-06-28
 ; PRIOR APPLICATION NUMBER: 60/302,591
 ; PRIOR FILING DATE: 2001-07-02
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 76
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Segment of xenla epithelial-cadherin precursor (e-cadherin)

US-10-185-815A-76

Query Match 46.9%; Score 23; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TAPP 5
|||
Db 4 TAPP 7

RESULT 47

US-07-841-662-31
; Sequence 31, Application US/07841662
; Patent No. 5314813
; GENERAL INFORMATION:
; APPLICANT: Peterson, Per A
; APPLICANT: Jackson, Michael
; APPLICANT: Lenglade-Demoyen, Pierre
; TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 No. 5314813th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/841.662
; FILING DATE: 19920219
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April

REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: SPFO001P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal

US-07-841-662-31

Query Match 46.9%; Score 23; DB 1; Length 9;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PVHNV 9
|||
Db 5 PVHGV 9

RESULT 48

US-08-209-797-31
; Sequence 31, Application US/08209797
; Patent No. 5529921
; GENERAL INFORMATION:

; APPLICANT: Peterson, Per A
; APPLICANT: Jackson, Michael
; APPLICANT: Lenglade-Demoyen, Pierre
; TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 No. 5529921th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/209,797
; FILING DATE: 10-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/841.662
; FILING DATE: 19-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Logan, April

REGISTRATION NUMBER: 33,950
; REFERENCE/DOCKET NUMBER: SPFO001P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal

US-08-209-797-31

Query Match 46.9%; Score 23; DB 1; Length 9;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PVHNV 9
|||
Db 5 PVHGV 9

RESULT 49

US-08-146-145-19
; Sequence 19, Application US/08146145
; Patent No. 5747269
; GENERAL INFORMATION:
; APPLICANT: Rammensee, Hans-Georg
; APPLICANT: Falk, Kirsten
; APPLICANT: R tzechke, Olaf
; APPLICANT: Stevanovic, Stefan
; APPLICANT: Jung, G nther
; TITLE OF INVENTION: DETERMINATION OF PEPTIDE MOTIFS ON MHC
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICANT: PatentIn Release #1.0, Version #1.25
;; FILING DATE: 17-NOV-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kitts, Monica C.
;; REGISTRATION NUMBER: 36.105
;; TELEPHONE: (202)638-5000
;; TELEFAX: (202)638-4810
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-146-145-19

Query Match 46.9%; Score 23; DB 1; Length 9;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PVHNV 9
Db 5 PVHGV 9

RESULT 50
US-08-669-685-31
;; Sequence 31, Application US/08669685
;; Patent No. 5827737
;; GENERAL INFORMATION:
;; APPLICANT: Peterson, Per A
;; APPLICANT: Jackson, Michael
;; APPLICANT: Lenglade-Demoyen, Pierre
;; TITLE OF INVENTION: IN VITRO ACTIVATION OF CYTOTOXIC T CELLS
;; NUMBER OF SEQUENCES: 36
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: The Scripps Research Institute
;; STREET: 10666 No. 5827737th Torrey Pines Road, TPC 8
;; CITY: La Jolla
;; STATE: California
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICANT: PatentIn Release #1.0, Version #1.25
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/209,797
;; FILING DATE: 10-MAR-1994
;; APPLICATION NUMBER: US 07/841,662
;; FILING DATE: 19-FEB-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Logan, April
;; REGISTRATION NUMBER: 33,950
;; REFERENCE/DOCKET NUMBER: SPF0001P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 554-2937
;; TELEFAX: (619) 554-6312
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid

;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
US-08-669-685-31

Query Match 46.9%; Score 23; DB 1; Length 9;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PVHNV 9
Db 5 PVHGV 9

Search completed: February 24, 2006, 10:19:37
Job time : 54 secs

This Page Blank (uspto)

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 24, 2006, 10:11:10 ; Search time 226 Seconds
(without alignments)
28.096 Million cell updates/sec

Title: US-10-019-513-1
Perfect score: 49
Sequence: 1 STAPPVHV 9

Scoring table: BL08UM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1766

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	42.9	8	2	Q05403 saccharomyc
2	18	36.7	8	1	FUSS_FUSSO
3	18	36.7	8	2	Q4VS04 MANSE
4	18	36.7	8	2	Q92205 HEPC
5	18	36.7	9	1	YBPR_AZOV
6	18	36.7	9	2	Q6SP94 CHLRE
7	18	36.7	9	2	Q99193 PSEPU
8	17	34.7	9	2	Q84U84 SOYBN
9	16	32.7	8	1	ALL6_CYPDO
10	16	32.7	8	2	Q6Y2F2 CITSI
11	16	32.7	8	2	Q7M067_MOUSE
12	16	32.7	9	2	Q9P8E5_KLUULA
13	16	32.7	9	2	Q71UR3_HUMAN
14	16	32.7	9	2	Q722E2_HUMAN
15	16	32.7	9	2	Q7YQC2_PANTR
16	16	32.7	9	2	Q7YQC3_PANTR
17	16	32.7	9	2	Q76FUI_9FLOR
18	16	32.7	9	2	Q76FUI_9FLOR
19	16	32.7	9	2	Q76FUI_9FLOR
20	16	32.7	9	2	Q76FV1_9FLOR
21	16	32.7	9	2	Q76FV1_9FLOR
22	16	32.7	9	2	Q64972_AVEVR
23	15	30.6	7	2	Q83492_BIOOC
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25	15	30.6	8	1	PPK2_PERAM
26	15	30.6	8	2	Q6J0R5_PARLI
27	15	30.6	8	2	Q7M1V6_SOLTU
28	15	30.6	9	2	Q8UCS8_HUMAN
29	15	30.6	9	2	Q16605_HUMAN
30	15	30.6	9	2	Q7M3S5_9TRYP
31	15	30.6	9	2	Q7R8X5_PLAYO

32	15	30.6	9	2	Q4X981_PLACH
33	15	30.6	9	2	Q4YFU0_PLABE
34	15	30.6	9	2	Q5G6L3_RIHA
35	15	30.6	9	2	Q81962_9FLOR
36	15	30.6	9	2	Q81964_9FLOR
37	15	30.6	9	2	Q81966_9FLOR
38	15	30.6	9	2	Q81968_9FLOR
39	15	30.6	9	2	Q6EU8 GERHY
40	15	30.6	9	2	Q76FS7_9FLOR
41	15	30.6	9	2	Q8HB43_9FLOR
42	15	30.6	9	2	Q8HB44_9FLOR
43	15	30.6	9	2	Q8HB45_GRACH
44	15	30.6	9	2	Q8HRJ8_9FLOR
45	15	30.6	9	2	Q8HRK0_9FLOR
46	15	30.6	9	2	Q8HSL0_9FLOR
47	15	30.6	9	2	Q8HSL5_9FLOR
48	15	30.6	9	2	Q8MDU2_9FLOR
49	15	30.6	9	2	Q8ME56_9RHOD
50	15	30.6	9	2	Q8ME58_9RHOD
51	15	30.6	9	2	Q8W7T9_BOSCA
52	15	30.6	9	2	Q8W875_BOSCA
53	15	30.6	9	2	Q8WU2_9FLOR
54	15	30.6	9	2	Q8T387_BOSRA
55	15	30.6	9	2	Q8T389_9FLOR
56	15	30.6	9	2	Q8TJ85_9FLOR
57	15	30.6	9	2	Q8TLD0_BOSMO
58	15	30.6	9	2	Q78337_9FLOR
59	15	30.6	9	2	Q71066_CANINE
60	15	30.6	9	2	Q82766_9PARA
61	15	30.6	9	2	Q90359_9POTY
62	14	28.6	7	1	TPFY_PACDA
63	14	28.6	7	1	UF04_MOUSE
64	14	28.6	7	2	P92210_AGROR
65	14	28.6	7	2	P92214_9POAL
66	14	28.6	7	2	P92218_9POAL
67	14	28.6	7	2	P92221_BROIN
68	14	28.6	7	2	P92226_CRIDE
69	14	28.6	7	2	P92372_9POAL
70	14	28.6	7	2	P92381_9POAL
71	14	28.6	7	2	P92385_HORMA
72	14	28.6	7	2	P92387_9POAL
73	14	28.6	7	2	P92390_HETPI
74	14	28.6	7	2	P92393_HORVU
75	14	28.6	7	2	P92403_LOPEL
76	14	28.6	7	2	P92421_PSAFR
77	14	28.6	7	2	P92425_PSEPI
78	14	28.6	7	2	P92427_9POAL
79	14	28.6	7	2	P92430_AEGTA
80	14	28.6	7	2	P92440_THIBE
81	14	28.6	7	2	P92442_TAECM
82	14	28.6	8	1	ALL5_CALVO
83	14	28.6	8	1	NGIF_RAT
84	14	28.6	8	2	Q13591_YEAST
85	14	28.6	8	2	Q6U7R2_CRYNV
86	14	28.6	8	2	Q699J0_BETVU
87	14	28.6	8	2	Q849P4_SALDE
88	14	28.6	8	2	Q84156_9POXV
89	14	28.6	9	1	BRK1_RANNI
90	14	28.6	9	1	FAR8_MACRS
91	14	28.6	9	1	KNL3_BOMVA
92	14	28.6	9	1	KNL3_CYPDO
93	14	28.6	9	2	Q7R5E8_PLAYO
94	14	28.6	9	2	Q4YFC4_PLABE
95	14	28.6	9	2	Q7M2M9_BOVIN
96	14	28.6	9	2	Q5IA44_SARAE
97	14	28.6	9	2	P82429_TOBAC
98	14	28.6	9	2	Q7YK04_9FABA
99	14	28.6	9	2	P82568_STRPY
100	14	28.6	9	2	P82568_STRPY
101	14	28.6	9	2	Q798K5_STRLI
102	14	28.6	9	2	Q8QRR5_9CORO
103	14	28.6	9	2	Q8QRR6_9CORO
104	14	28.6	9	2	Q8QRR6_9CORO

Q4X981	plasmodium
Q4YFU0	plasmodium
Q5G6L3	rhinopoma h
Q81962	caloglossa
Q81964	caloglossa
Q81966	caloglossa
Q81968	caloglossa
Q6EU8	gerbera hyb
Q76FS7	hypnea japo
Q8HB43	gracilaria
Q8HB44	gracilaria
Q8HB45	gracilaria
Q8HRJ8	ptilophora
Q8HRK0	gracilaria
Q8HSL0	murrayella
Q8HSL5	spyridia fi
Q8MDU2	hypnea sp
Q8ME56	porphyra mi
Q8ME58	porphyra li
Q8W7T9	bostrychia
Q8W875	bostrychia
Q8WU2	bostrychia
Q8T387	bostrychia
Q8T389	caloglossa
Q8TJ85	caloglossa
Q8TLD0	bostrychia
Q78337	caloglossa
Q71066	canine dist
Q82766	canine dist
P90359	barley mild
P83455	pachymedusa
P83462	mus musculus
P92210	agropyron c
P92214	amblyopyrum
P92218	australopyr
P92221	bromus iner
P92226	crithopsis
P92372	haynaldia v
P92381	hordeum bra
P92385	hordeum mar
P92387	henradia p
P92390	heteranthel
P92393	hordeum vul
P92403	lophopyrum
P92421	psathyrosta
P92425	pseudoroegn
P92427	peridictyon
P92430	aegilops ta
P92440	thinopyrum
P92442	taeniatheru
P41841	calliphora
P82598	rattus norv
Q13591	saccharomyc
Q6U7R2	cryptococcu
Q699J0	beta vulgar
Q849P4	salmonella
Q84156	orf virus
Q71254	rana nigrom
P82281	macrobrachi
P83058	combina var
P83659	cyphononyx
Q9TWV0	anthopleura
Q7re58	plasmodium
Q4YFC4	plasmodium
Q7M2M9	bos taurus
Q5IA44	philodendro
P82429	nicotiana t
Q7YK04	acacia berl
Q9MVU1	caloglossa
P82568	streptococc
Q798K5	streptomyce
Q8QRR5	transmissib
Q8QRR6	transmissib

105	14	28.6	9	2	P84497	trachemys s	P84497	178	12	24.5	9	2	Q7JIS9	LACAG	Q7JIS9	lagenorhync
106	14	28.6	9	2	Q6I754	cynops pyrr	Q6I754	179	12	24.5	9	2	Q7JIT0	LACAG	Q7JIT0	lagenorhync
107	14	28.6	9	2	Q7LZ50	gallus gall	Q7LZ50	180	12	24.5	9	2	Q7JIT1	LACAG	Q7JIT1	lagenorhync
108	14	28.6	9	2	Q7LZJ8	rana tempor	Q7LZJ8	181	12	24.5	9	2	Q9GJVI	LACAG	Q9GJVI	lagenorhync
109	14	28.6	9	2	Q9PRJ4	lepisosteus	Q9PRJ4	182	12	24.5	9	2	Q9GJV2	LACAG	Q9GJV2	lagenorhync
110	14	28.6	9	2	Q7LZJ7	heleophryne	Q7LZJ7	183	12	24.5	9	2	Q9GJV3	LACAG	Q9GJV3	lagenorhync
111	13	26.5	6	1	MAP SCHMA	schistosoma	P84575	184	12	24.5	9	2	Q5DQJ7	9LILI	Q5DQJ7	nenga pumil
112	13	26.5	7	1	CHOX ALCSP	alcaligenes	P16101	185	12	24.5	9	2	Q5DQK7	9LILI	Q5DQK7	hydriastele
113	13	26.5	7	1	UC24_MAIZE	zea mays (m	P86630	186	12	24.5	9	2	Q5DQK6	9LILI	Q5DQK6	gronophyllu
114	13	26.5	7	2	Q50556 ACTAC	Q50556 actinobacil	O50556	187	12	24.5	9	2	Q5DQK8	9LILI	Q5DQK8	gronophyllu
115	13	26.5	7	2	Q8RMS3_9ENTR	klebsiella	K8RMS3	188	12	24.5	9	2	Q5DQK0	9LILI	Q5DQK0	gronophyllu
116	13	26.5	8	2	Q9T2W0_YEAST	Q9T2W0 saccharomyc	Q9T2W0	189	12	24.5	9	2	Q5DQK4	9LILI	Q5DQK4	areca rheop
117	13	26.5	8	2	Q6LD47_HUMAN	Q6LD47 homo sapien	Q6LD47	190	12	24.5	9	2	Q5DQK6	9LILI	Q5DQK6	areca catec
118	13	26.5	8	2	Q42507_WHEAT	Q42507 triticum ae	Q42507	191	12	24.5	9	2	Q5DQK1	9LILI	Q5DQK1	manicaria s
119	13	26.5	8	2	Q8LB02_MAIZE	Q8LB02 zea mays (m	Q8LB02	192	12	24.5	9	2	Q5DQK2	9LILI	Q5DQK2	leopoldinia
120	13	26.5	8	2	P8J352_LACSN	P8J352 lactobacill	P8J352	193	12	24.5	9	2	Q5DQF3	9LILI	Q5DQF3	kentloopsis
121	13	26.5	8	2	Q7X4Q5_NODSP	Q7X4Q5 nodularia s	Q7X4Q5	194	12	24.5	9	2	Q5DQK4	9LILI	Q5DQK4	iguanura wa
122	13	26.5	8	2	Q9R9E0_BACSU	Q9R9E0 bacillus su	Q9R9E0	195	12	24.5	9	2	Q5DQK6	9LILI	Q5DQK6	amandira de
123	13	26.5	8	2	Q90345_9FLAV	Q90345 gb virus c/	O90345	196	12	24.5	9	2	Q70Y80	9LAMI	Q70Y80	plectranthu
124	13	26.5	9	1	PVK2_MUSDO	musca domes	P84355	197	12	24.5	9	2	Q70Y82	9LAMI	Q70Y82	alvesia ros
125	13	26.5	9	2	Q67AQ6_HUMAN	Q67AQ6 homo sapien	Q67AQ6	198	12	24.5	9	2	Q6VFK2	VIBFI	Q6VFK2	vibrio fisc
126	13	26.5	9	2	Q67AR0_HUMAN	Q67AR0 homo sapien	Q67AR0	199	12	24.5	9	2	Q9R7H9	HABIN	Q9R7H9	haemophilus
127	13	26.5	9	2	Q67AR1_HUMAN	Q67AR1 homo sapien	Q67AR1	200	12	24.5	9	2	Q7M0H1	MOUSE	Q7M0H1	mus musculu
128	13	26.5	9	2	Q67AS0_HUMAN	Q67AS0 homo sapien	Q67AS0	201	12	24.5	9	2	Q8CG39	RAT	Q8CG39	rattus norv
129	13	26.5	9	2	Q67AS3_HUMAN	Q67AS3 homo sapien	Q67AS3	202	12	24.5	9	2	Q50L10	XENLA	Q50L10	xenopus lae
130	13	26.5	9	2	Q7WRU6_NODSP	Q7WRU6 nodularia s	Q7WRU6	203	12	24.5	9	2	Q4VN46	FUGRU	Q4VN46	fugu rubrip
131	12	24.5	5	1	EIO3_LITRU	EIO3 littoria rub	P82099	204	11	22.4	4	1	TUFT_HUMAN		TUFT_HUMAN	homo sapien
132	12	24.5	5	1	EIO4_LITRU	EIO4 littoria rub	P82100	205	11	22.4	4	1	YLM1_YEAST		YLM1_YEAST	homo sapien
133	12	24.5	5	1	SUGA_ACHDO	P19991 acheta dome	P19991	206	11	22.4	5	1	BP77_BOTIN		BP77_BOTIN	saccharomyc
134	12	24.5	8	1	ALL1_CVDPO	P82152 cydia pomon	P82152	207	11	22.4	6	1	CIP2_MYTED		CIP2_MYTED	bothrops in
135	12	24.5	8	1	KIN15_PERAM	P82689 periplaneta	P82689	208	11	22.4	7	2	P72081	NOCLA	P72081	mytilus edu
136	12	24.5	8	1	LCK1_LEUPHA	P21140 leucophaea	P21140	209	11	22.4	7	2	Q8MF76	9ASTR	Q8MF76	taraxacum (
137	12	24.5	8	2	Q7Z6G0_HUMAN	Q7Z6G0 homo sapien	Q7Z6G0	210	11	22.4	7	2	Q66205	9CORO	Q66205	nocardia la
138	12	24.5	8	2	Q9BY5_HUMAN	Q9BY5 homo sapien	Q9BY5	211	11	22.4	8	1	ANGT2	BOTJA	Q62082	transmiseib
139	12	24.5	8	2	Q9UHK1_HUMAN	Q9UHK1 homo sapien	Q9UHK1	212	11	22.4	8	1	B44K_PORGI		B44K_PORGI	bothrops ja
140	12	24.5	8	2	Q53TM6_HUMAN	Q53TM6 homo sapien	Q53TM6	213	11	22.4	8	1	CAP4_CANAL		CAP4_CANAL	porphyromon
141	12	24.5	8	2	Q28866_MEGNO	Q28866 megaptera n	Q28866	214	11	22.4	8	1	CLP_THICU		CLP_THICU	candida alb
142	12	24.5	8	2	Q9BP99_HYICO	Q9BP99 hylobates c	Q9BP99	215	11	22.4	8	1	FAR4_MACRS		FAR4_MACRS	thiobacillu
143	12	24.5	8	2	Q9BFA0_MACMU	Q9BFA0 macaca mula	Q9BFA0	216	11	22.4	8	1	RS7_MYCIT		RS7_MYCIT	macrobachi
144	12	24.5	8	2	Q9GMH3_LACOB	Q9GMH3 lagenorhync	Q9GMH3	217	11	22.4	8	1	UPAI_HUMAN		UPAI_HUMAN	mycobacteri
145	12	24.5	8	2	Q9TT78_CANFA	Q9TT78 canis fami	Q9TT78	218	11	22.4	8	2	P82858	9BASI	P82858	homo sapien
146	12	24.5	8	2	Q5DQK1_9LILI	Q5DQK1 loxococcus	Q5DQK1	219	11	22.4	8	2	Q96QF9	HUMAN	Q96QF9	puccinia re
147	12	24.5	8	2	Q5DQK8_9LILI	Q5DQK8 hydriastele	Q5DQK8	220	11	22.4	8	2	Q96QF9	HUMAN	Q96QF9	homo sapien
148	12	24.5	8	2	Q5DQK2_9LILI	Q5DQK2 gulubia cos	Q5DQK2	221	11	22.4	8	2	O02032	LYTPI	O02032	lytechinus
149	12	24.5	8	2	Q5DQK7_9LILI	Q5DQK7 gronophyllu	Q5DQK7	222	11	22.4	8	2	Q8MUN6	9NEOP	Q8MUN6	heliconius
150	12	24.5	8	2	Q5DQK2_9LILI	Q5DQK2 gronophyllu	Q5DQK2	223	11	22.4	8	2	QSTRX8	BOVIN	QSTRX8	bos taurus
151	12	24.5	8	2	Q5DQK2_9LILI	Q5DQK2 gronophyllu	Q5DQK2	224	11	22.4	8	2	Q70KG9	PIG	Q70KG9	sus scrofa
152	12	24.5	8	2	Q5DQK3_9LILI	Q5DQK3 areca trian	Q5DQK3	225	11	22.4	8	2	O19957	GOSHI	O19957	gossypium h
153	12	24.5	8	2	Q5DQK5_9LILI	Q5DQK5 cyphosperma	Q5DQK5	226	11	22.4	8	2	Q7M1U0	ORYSA	Q7M1U0	oryza sativ
154	12	24.5	8	2	Q6Z269_9CARY	Q6Z269 silene ajan	Q6Z269	227	11	22.4	8	2	Q9MSX1	9ASTR	Q9MSX1	jurinea hum
155	12	24.5	8	2	Q70Y68_9LAMI	Q70Y68 prostanther	Q70Y68	228	11	22.4	8	2	Q9SB24	TOBAC	Q9SB24	nicotiana t
156	12	24.5	8	2	Q70Y88_9LAMI	Q70Y88 platostoma	Q70Y88	229	11	22.4	8	2	Q4QYN7	9POAL	Q4QYN7	saccharum s
157	12	24.5	8	2	P8J158_ANASL	P8J158 anabaena sp	P8J158	230	11	22.4	8	2	Q4QYN9	9POAL	Q4QYN9	saccharum e
158	12	24.5	8	2	Q934S4_THIFE	Q934S4 thiobacillu	Q934S4	231	11	22.4	8	2	Q4QYP2	9POAL	Q4QYP2	saccharum s
159	12	24.5	8	2	Q9RQ49_9ENTR	Q9RQ49 buchnera ap	Q9RQ49	232	11	22.4	8	2	Q4QYP3	9POAL	Q4QYP3	saccharum b
160	12	24.5	8	2	Q9RQ57_9ENTR	Q9RQ57 buchnera ap	Q9RQ57	233	11	22.4	8	2	Q4QYP5	9POAL	Q4QYP5	saccharum r
161	12	24.5	8	2	Q44463_9RHIZ	Q44463 rhizobiales	Q44463	234	11	22.4	8	2	Q4QYP6	SACOF	Q4QYP6	saccharum o
162	12	24.5	8	2	Q5G852_9GRUI	Q5G852 aramides yp	Q5G852	235	11	22.4	8	2	Q56246	BACPF	Q56246	bacillus ps
163	12	24.5	8	2	Q90498_ERYGO	Q90498 erythrura g	Q90498	236	11	22.4	8	2	Q5M6L9	CAMJE	Q5M6L9	campylobact
164	12	24.5	8	2	Q91098_MANME	Q91098 manorina me	Q91098	237	11	22.4	8	2	Q7M0L0	CLOST	Q7M0L0	clostridium
165	12	24.5	9	1	ALC_CHIRE	Q6VMC6 serilophus	Q6VMC6	238	11	22.4	8	2	Q7M041	RAT	Q7M041	rattus norv
166	12	24.5	9	1	BSF43_SERPL	P83678 chlamydomon	P83678	239	11	22.4	8	2	Q8K327	MOUSE	Q8K327	mus musculu
167	12	24.5	9	1	CB22_SPIOL	P83375 serratia pl	P83375	240	11	22.4	8	2	Q5XPV7	MOUSE	Q5XPV7	mus musculu
168	12	24.5	9	1	FLAA2_TREHY	P80159 spinacia ol	P80159	241	11	22.4	8	2	Q89496	9CORO	Q89496	murine hepa
169	12	24.5	9	2	Q7M471_VESOR	P80159 treponema h	P80159	242	11	22.4	8	2	Q641X4	FUNHE	Q641X4	fundulus he
170	12	24.5	9	2	Q9TWX7_MANSE	Q9TWX7 vespa orien	Q9TWX7	243	11	22.4	8	2	Q8AWV7	ANAPL	Q8AWV7	anas platyr
171	12	24.5	9	2	Q7RBUE_PLAYO	Q7RBUE manduca sex	Q7RBUE	244	11	22.4	8	2	Q8AWV8	9AVES	Q8AWV8	cygnus colu
172	12	24.5	9	2	Q7JIS3_LACOB	Q7JIS3 plasmodium	Q7JIS3	245	11	22.4	8	2	Q8AWV9	ANSCC	Q8AWV9	anser caeru
173	12	24.5	9	2	Q7JIS4_LAGOL	Q7JIS4 lagenorhync	Q7JIS4	246	11	22.4	8	2	Q8AWW0	COSCO	Q8AWW0	coscoroba c
174	12	24.5	9	2	Q7JIS5_LAGOL	Q7JIS5 lagenorhync	Q7JIS5	247	11	22.4	8	2	Q4FUM5	9CICH	Q4FUM5	lepidolamp
175	12	24.5	9	2	Q7JIS6_LAGOL	Q7JIS6 lagenorhync	Q7JIS6	248	11	22.4	8	2	Q85562	MLVMO	Q85562	moloney mur
176	12	24.5	9	2	Q7JIS7_LAGOL	Q7JIS7 lagenorhync	Q7JIS7	249	11	22.4	9	1	ALL10_CARMA		ALL10_CARMA	carcinus ma
177	12	24.5	9	2	Q7JIS8_LAGOL	Q7JIS8 lagenorhync	Q7JIS8	250	11	22.4	9	1	FAR2_PANRE		FAR2_PANRE	panagrellus
													FAR5_CALVO		FAR5_CALVO	calliphora

397	10	20.4	9	2	Q765Y9_CHICK	Q765Y9_gallus gall	470	9	18.4	8	2	Q7M1C5_ACIFE	Q7m1c5_acidaminoco
398	10	20.4	9	2	Q4PU39_9CICH	Q4pu39_lepiditolamp	471	9	18.4	8	2	Q8G940_BORBU	Q8g940_borrelia bu
399	9	18.4	5	1	BIOB_CITPR	P12997_citrobacter	472	9	18.4	8	2	Q9S5L7_CLOTH	Q9s5l7_clostridium
400	9	18.4	6	1	PYF1_PENNO	P84005_pennaeus mon	473	9	18.4	8	2	Q9S6D5_ECOLI	Q9s6d5_escherichia
401	9	18.4	6	1	TWOF_SARBU	P41495_sarcophaga	474	9	18.4	8	2	Q62933_RAT	Q62933_rattus norv
402	9	18.4	7	1	E105_LITRU	P82101_litoria rub	475	9	18.4	8	2	Q78DX6_RAT	Q78dx6_rattus norv
403	9	18.4	7	1	HV7_FIG	P01153_sus scrofa	476	9	18.4	8	2	Q9JLD7_MESAU	Q9jld7_mesocricetu
404	9	18.4	7	2	Q98866_SPIOL	O98866_spinacia ol	477	9	18.4	8	2	Q9QVK5_MURI	Q9qvk5_rattus ep.
405	9	18.4	7	2	Q8GL04_BORBU	Q8gl04_borrelia bu	478	9	18.4	8	2	Q5QNV0_MOUSE	Q5qnv0_mus musculu
406	9	18.4	7	2	Q8GL12_BORBU	Q8gl12_borrelia bu	479	9	18.4	8	2	Q35835_MURI	Q35835_rattus ep.
407	9	18.4	7	2	P70804_AZOVI	P70804_azotobacter	480	9	18.4	8	2	Q62527_MUSSP	Q62527_mus spretus
408	9	18.4	7	2	Q65578_9ALPH	Q65578_bovine herp	481	9	18.4	8	2	Q80WD5_MUSSP	Q80wd5_mus spretus
409	9	18.4	7	2	Q67113_9INEA	Q67113_influenza a	482	9	18.4	8	2	Q5YDB9_9PERC	Q5ydb9_xiphister m
410	9	18.4	7	2	Q07624_9RETR	Q07624_rous sarcom	483	9	18.4	8	2	Q715L5_VARDU	Q715l5_varanus dum
411	9	18.4	7	2	Q8UE81_9HIVI	Q8ue81_human immun	484	9	18.4	8	2	Q94V88_9SAUR	Q94v88_varanus tri
412	9	18.4	8	1	AXHG_GRYBI	P67785_gryllus bim	485	9	18.4	8	2	Q94V91_VARTI	Q94v91_varanus tim
413	9	18.4	8	1	AXH_PROTE	P61856_protophormi	486	9	18.4	8	2	Q94VA0_9SAUR	Q94va0_varanus sem
414	9	18.4	8	1	AXH_ROMMI	P67786_romalea mic	487	9	18.4	8	2	Q94VA7_9SAUR	Q94va7_varanus eal
415	9	18.4	8	1	AXH_TABAT	P14595_tabanus atr	488	9	18.4	8	2	Q94VB2_9SAUR	Q94vb2_varanus eal
416	9	18.4	8	1	ALL12_CARMA	P81815_carcinus ma	489	9	18.4	8	2	Q94VB5_9SAUR	Q94vb5_varanus eal
417	9	18.4	8	1	ALL15_CARMA	P81818_carcinus ma	490	9	18.4	8	2	Q94VB4_VARMML	Q94vb4_varanus mel
418	9	18.4	8	1	ALL4_CYPDO	P81155_cydia pomon	491	9	18.4	8	2	Q94VF3_9SAUR	Q94vf3_varanus kei
419	9	18.4	8	1	ALL8_CARMA	P81811_carcinus ma	492	9	18.4	8	2	Q94VF9_VARIN	Q94vf9_varanus ind
420	9	18.4	8	1	C125_CYPDO	P83661_cyphononyx	493	9	18.4	8	2	Q94VJ4_VARBIN	Q94vj4_varanus ben
421	9	18.4	8	1	DY55_LIMS	P82083_limnodynast	494	9	18.4	8	2	Q76VD6_BLV	Q76vd6_bovine leuk
422	9	18.4	8	1	PAR7_ASCSU	P43171_ascaris suu	495	9	18.4	9	1	CB2B_SFOL	Q92l10_spinacia ol
423	9	18.4	8	1	GLOR_HUMAN	P02729_homo sapien	496	9	18.4	9	1	CCAP_CARMA	P84119_carcinus ma
424	9	18.4	8	1	HTF2_BLAOR	P84258_biatta orie	497	9	18.4	9	1	CCAP_SPOER	P84121_spodoptera
425	9	18.4	8	1	HTF2_LEPDE	P84257_leptinotars	498	9	18.4	9	1	CCAP_TENNO	P84120_tenebrio mo
426	9	18.4	8	1	HTF2_PERAM	P84256_periplaneta	499	9	18.4	9	1	CONO_CONGE	P05486_conus geogr
427	9	18.4	8	1	LCK4_LEUMA	P21143_leucophaea	500	9	18.4	9	1	CONO_CONST	P05487_conus stria
428	9	18.4	8	1	LCK6_LEUMA	P19988_leucophaea	501	9	18.4	9	1	NEUI_BALPH	P69056_balaenopter
429	9	18.4	8	1	LPK_LEUMA	P13049_leucophaea	502	9	18.4	9	1	NEUI_HIPAM	P69044_hippopotamu
430	9	18.4	8	1	LPMS_STARP	P23211_staphylococ	503	9	18.4	9	1	NEUI_RABIT	P69043_cryptocolagus
431	9	18.4	8	1	TXV1_PHONI	Q7m3p1_phonotria	504	9	18.4	9	1	NEUI_TACAC	P69057_tachyglossus
432	9	18.4	8	1	UF06_MOUSE	P38644_mus musculu	505	9	18.4	9	1	OXYT_CYPCA	P69058_hydrolagus
433	9	18.4	8	2	Q7LIH2_YEAST	P71ih2_saccharomyc	506	9	18.4	9	1	OXYT_HYDCA	P69128_cypripus ca
434	9	18.4	8	2	Q15889_HUMAN	Q15889_homo sapien	507	9	18.4	9	1	OXYT_PETMA	P69129_petrymazon
435	9	18.4	8	2	Q33ST6_HUMAN	Q53st6_homo sapien	508	9	18.4	9	1	PKK1_PERAM	P82691_periplaneta
436	9	18.4	8	2	Q5BR65_SCHJA	Q5br65_schistosoma	509	9	18.4	9	1	PFY4_PENNO	P84008_pennaeus mon
437	9	18.4	8	2	Q6VYE3_TNEOP	Q6vye3_heliconius	510	9	18.4	9	1	PFY4_PENNO	P84004_loligo vulg
438	9	18.4	8	2	Q70MX3_TRYBR	Q70mx3_trypanosoma	511	9	18.4	9	1	PFY4_PENNO	P82926_bos taurus
439	9	18.4	8	2	Q7M3N2_MANSE	Q7m3n2_manduca sex	512	9	18.4	9	1	RT33_BOVIN	P19149_streptomyce
440	9	18.4	8	2	Q8GCD7_9EUCA	Q8gcd7_lomis hirta	513	9	18.4	9	1	XVLA_STRS8	P19149_streptomyce
441	9	18.4	8	2	Q4X617_PLACH	Q4x617_plasmodium	514	9	18.4	9	2	Q15891_HUMAN	Q15891_homo sapien
442	9	18.4	8	2	Q4XT27_PLACH	Q4xt27_plasmodium	515	9	18.4	9	2	Q15896_HUMAN	Q15896_homo sapien
443	9	18.4	8	2	Q95213_RABIT	Q95213_cryptocolagus	516	9	18.4	9	2	Q8IUU5_HUMAN	Q8iuu5_homo sapien
444	9	18.4	8	2	Q9TRY3_9CETA	Q9try3_sus sp. ins	517	9	18.4	9	2	Q9H326_HUMAN	Q9h326_homo sapien
445	9	18.4	8	2	Q8H9K1_9CAUD	Q8h9k1_bacterioph	518	9	18.4	9	2	Q9UC36_HUMAN	Q9uc36_homo sapien
446	9	18.4	8	2	Q88BU0_BPR69	Q88bjo_bacterioph	519	9	18.4	9	2	Q9UKJ6_HUMAN	Q9ukj6_homo sapien
447	9	18.4	8	2	O19956_GOSAR	O19956_gossypium a	520	9	18.4	9	2	Q9UMA0_HUMAN	Q9uma0_homo sapien
448	9	18.4	8	2	O19958_GOSBA	O19958_gossypium b	521	9	18.4	9	2	Q9UQW0_HUMAN	Q9uqw0_homo sapien
449	9	18.4	8	2	O19959_GOSTO	O19959_gossypium m	522	9	18.4	9	2	Q5C1F8_SCHJA	Q5c1f8_schistosoma
450	9	18.4	8	2	O19960_GOSMU	O19960_gossypium m	523	9	18.4	9	2	P84502_9ANNE	P84502_annelida. l
451	9	18.4	8	2	O19961_GOSDA	O19961_gossypium d	524	9	18.4	9	2	Q7RR12_PLAYO	Q7rr12_plasmodium
452	9	18.4	8	2	Q40659_ORYSA	Q40659_oryza sativ	525	9	18.4	9	2	Q8WGB6_PROCL	Q8wgb6_procambarus
453	9	18.4	8	2	Q5D4X1_9MYRT	Q5d4x1_physocalymm	526	9	18.4	9	2	Q4YER1_PLABE	Q4yer1_plasmodium
454	9	18.4	8	2	Q5D4X2_9MYRT	Q5d4x2_pehria comp	527	9	18.4	9	2	Q4YIG1_PLABE	Q4yig1_plasmodium
455	9	18.4	8	2	Q5D4X4_9MYRT	Q5d4x4_koehneria m	528	9	18.4	9	2	Q28093_BOVIN	Q28093_bos taurus
456	9	18.4	8	2	Q659Q3_9CARY	Q659q3_silene oste	529	9	18.4	9	2	Q6LAP5_WACEU	Q6lap5_macropus eu
457	9	18.4	8	2	Q659Q5_9CARY	Q659q5_silene invo	530	9	18.4	9	2	Q9XJNO_9VIRU	Q9xjno_bacterioph
458	9	18.4	8	2	Q70Y57_9LAMI	Q70y57_fuerstia af	531	9	18.4	9	2	Q58U35_FESSE	Q58u35_festucopsis
459	9	18.4	8	2	Q7XB03_MAIZE	Q7xb03_zea mays (m	532	9	18.4	9	2	Q58U41_9FOAL	Q58u41_haynaldia r
460	9	18.4	8	2	Q9GD00_9JILI	Q9gd00_masoala mad	533	9	18.4	9	2	Q5D4X3_9MYRT	Q5d4x3_lourtellia r
461	9	18.4	8	2	Q9SAY7_9TILI	Q9say7_dioscorea t	534	9	18.4	9	2	Q70Y63_CONTO	Q70y63_congea tome
462	9	18.4	8	2	Q4JLA6_BETVU	Q4jla6_beta vulgar	535	9	18.4	9	2	Q76FU3_9FLOR	Q76fu3_plocamium t
463	9	18.4	8	2	Q68485_KLEPN	Q68485_klebsiella	536	9	18.4	9	2	Q76FU9_9FLOR	Q76fu9_plocamium r
464	9	18.4	8	2	P72221_PRESP	P72221_pseudomonas	537	9	18.4	9	2	Q7X8P7_MAIZE	Q7x8p7_zea mays (m
465	9	18.4	8	2	P77556_ECOLI	P77556_escherichia	538	9	18.4	9	2	Q30790_ERWAM	Q30790_erwinia amy
466	9	18.4	8	2	Q56140_STRTR	Q56140_streptococc	539	9	18.4	9	2	Q43928_AGRPU	Q43928_aeromonas p
467	9	18.4	8	2	P83152_ANASL	P83152_anabaena sp	540	9	18.4	9	2	Q44001_9GAMM	Q44001_aeromonas e
468	9	18.4	8	2	Q6LDP8_PSEAE	Q6ldp8_pseudomonas	541	9	18.4	9	2	Q44377_AERTR	Q44377_aeromonas t
469	9	18.4	8	2	Q7DKL7_STAUA	Q7dkl7_staphylococ	542	9	18.4	9	2	Q44468_9GAMM	Q44468_aeromonas v

543	9	18.4	9	2	Q57328_AERSO	Q57328 aeromonas s	616	8	16.3	8	2	Q9UDZ4_HUMAN	Q9UDZ4 homo sapien
544	9	18.4	9	2	Q61AR8_AERHY	Q61AR8 aeromonas h	617	8	16.3	8	2	Q9UMH9_HUMAN	Q9UMH9 homo sapien
545	9	18.4	9	2	Q8G1Z6_LACDL	Q8G1Z6 lactobacill	618	8	16.3	8	2	Q34909_LOCOMI	Q34909 locusta mig
546	9	18.4	9	2	Q8GLZ6_BORBU	Q8GLZ6 borrelia bu	619	8	16.3	8	2	Q9UB13_PULM	Q9UB13 albinaria h
547	9	18.4	9	2	Q8BKU3_BORBU	Q8BKU3 borrelia bu	620	8	16.3	8	2	Q4XU8_PLACH	Q4XU8 plasmodium
548	9	18.4	9	2	Q9JN16_STRPY	Q9JN16 streptococc	621	8	16.3	8	2	Q02831_RABIT	Q02831 rhyctolagus
549	9	18.4	9	2	Q9R635_CHUTR	Q9R635 chlamydia t	622	8	16.3	8	2	Q9BF82_URSA	Q9BF82 urus arcto
550	9	18.4	9	2	Q9R635_BORBU	Q9R635 borrelia bu	623	8	16.3	8	2	Q9BF83_CANFA	Q9BF83 canis fami
551	9	18.4	9	2	Q47556_ECOLI	Q47556 bacillus su	624	8	16.3	8	2	Q9BF84_PANON	Q9BF84 panthera on
552	9	18.4	9	2	Q84F20_BACSU	Q84F20 bacillus su	625	8	16.3	8	2	Q9BF85_LEOPA	Q9BF85 leopardus p
553	9	18.4	9	2	Q31363_BORGA	Q31363 borrelia ga	626	8	16.3	8	2	Q9BF86_FELCA	Q9BF86 felis silve
554	9	18.4	9	2	Q924N8_MOUSE	Q924N8 mus musculu	627	8	16.3	8	2	Q9BF87_TAPIN	Q9BF87 tapirus ind
555	9	18.4	9	2	Q61723_MOUSE	Q61723 mus musculu	628	8	16.3	8	2	Q9BF88_EQUSC	Q9BF88 equus cabal
556	9	18.4	9	2	Q71069_9PARA	Q71069 canine dist	629	8	16.3	8	2	Q9BF89_OKAJO	Q9BF89 okapia joh
557	9	18.4	9	2	Q69473_HV1	Q69473 human herpe	630	8	16.3	8	2	Q9BF90_TRAEU	Q9BF90 tragelaphu
558	9	18.4	9	2	Q82622_9COCO	Q82622 avian infec	631	8	16.3	8	2	Q9BF91_HIPAM	Q9BF91 hippopotamu
559	9	18.4	9	2	Q31415_CHICK	Q31415 gallus gall	632	8	16.3	8	2	Q9BF94_NYCTH	Q9BF94 nycteris th
560	9	18.4	9	2	Q6HA63_TRITG	Q6HA63 trimeresuru	633	8	16.3	8	2	Q9BF95_ROULA	Q9BF95 rousettus l
561	9	18.4	9	2	Q6HA76_9SAUR	Q6HA76 trimeresuru	634	8	16.3	8	2	Q9BF96_PTEGI	Q9BF96 pteropus gi
562	9	18.4	9	2	Q71DX2_9SAUR	Q71DX2 urostephous	635	8	16.3	8	2	Q9BF97_ARTJA	Q9BF97 artibeus ja
563	9	18.4	9	2	Q71Z81_RANPI	Q71Z81 rana pipien	636	8	16.3	8	2	Q9BF98_CALGO	Q9BF98 callimico g
564	9	18.4	9	2	Q8SHF0_CHANA	Q8SHF0 chamaeleo n	637	8	16.3	8	2	Q9BFA1_ATEFU	Q9BFA1 ateleus fusc
565	9	18.4	9	2	Q94VC6_9SAUR	Q94VC6 varanus pil	638	8	16.3	8	2	Q9BFA2_TARBA	Q9BFA2 tarsius ban
566	9	18.4	9	2	Q94VJ1_VARDO	Q94VJ1 varanus dor	639	8	16.3	8	2	Q9BFA3_LEMCA	Q9BFA3 lemur catia
567	9	18.4	9	2	Q9PS68_CHICK	Q9PS68 gallus gall	640	8	16.3	8	2	Q9BFA4_TUPMI	Q9BFA4 tupaia mino
568	9	18.4	9	2	Q9T688_GECGE	Q9T688 gekko gekko	641	8	16.3	8	2	Q9BFA5_CYNVA	Q9BFA5 cynocephalu
569	9	18.4	9	2	Q53EB6_9NEOB	Q53EB6 eleutheroda	642	8	16.3	8	2	Q9BFA6_ORYAF	Q9BFA6 orycteropus
570	9	18.4	9	2	Q4TU46_9AVES	Q4TU46 anser anser	643	8	16.3	8	2	Q9BFA8_LOXAF	Q9BFA8 loxia a
571	9	18.4	9	2	Q8AEW8_9HIV1	Q8AEW8 human immun	644	8	16.3	8	2	Q9BFA9_PROCA	Q9BFA9 procavia ca
572	8	16.3	8	1	GRWV_HUMAN	P01157 homo sapien	645	8	16.3	8	2	Q9BFB0_TRIMA	Q9BFB0 trichechus
573	8	16.3	8	1	THYL_BOMOR	P62970 bombina ori	646	8	16.3	8	2	Q9BFB1_ECHTE	Q9BFB1 echinops te
574	8	16.3	3	1	THYL_NOTVI	P62971 notophthalm	647	8	16.3	8	2	Q9BFB2_SORAR	Q9BFB2 sorex arane
575	8	16.3	3	1	THYL_PIG	P62969 sus scrofa	648	8	16.3	8	2	Q9BFB3_CONCR	Q9BFB3 condylura c
576	8	16.3	3	1	THYL_SHEEP	P62969 ovis aries	649	8	16.3	8	2	Q9BFB4_TALAL	Q9BFB4 talpa alta
577	8	16.3	3	1	DCML_PSECH	P19316 pseudomonas	650	8	16.3	8	2	Q9BFB5_ERICO	Q9BFB5 erinaceus c
578	8	16.3	5	1	FARP_CHICK	P83308 gallus gall	651	8	16.3	8	2	Q9BFB6_MYRTE	Q9BFB6 myrmecophag
579	8	16.3	5	1	TPIS_CANFA	P54714 canis fami	652	8	16.3	8	2	Q9BFB7_TAMAND	Q9BFB7 tamandua te
580	8	16.3	5	2	Q99007_HORVU	Q99007 hordeum vul	653	8	16.3	8	2	Q9BFB8_CHAVI	Q9BFB8 chaetophrac
581	8	16.3	6	1	ASP2_LACSN	P82655 lactobacill	654	8	16.3	8	2	Q9BFB9_EUPSX	Q9BFB9 euphractur
582	8	16.3	6	1	CIP1_MYTED	P13736 mytilus edu	655	8	16.3	8	2	Q9BFC0_CHODI	Q9BFC0 choleopus d
583	8	16.3	7	1	FAP2_ASCSU	P67879 ascaris suu	656	8	16.3	8	2	Q9BFC1_CHOHO	Q9BFC1 choleopus h
584	8	16.3	7	1	FAP2_PANRE	P67880 panagrellus	657	8	16.3	8	2	Q9BFC2_MACEU	Q9BFC2 macropus eu
585	8	16.3	7	1	LANC_CARUI	P36960 carnobacter	658	8	16.3	8	2	Q9BFC3_DIDMA	Q9BFC3 didelphis m
586	8	16.3	7	1	MNP1_LEPDE	P42984 leptinotars	659	8	16.3	8	2	Q9XSV1_CANFA	Q9XSV1 canis fami
587	8	16.3	7	1	UF03_MOUSE	P38641 mus musculu	660	8	16.3	8	2	Q6SKV2_9NARC	Q6SKV2 trichocolea
588	8	16.3	7	2	Q8TAQ4_HUMAN	Q8TAQ4 homo sapien	661	8	16.3	8	2	Q76414_CVCPA	Q76414 cycas panch
589	8	16.3	7	2	P93233_LYCES	P93233 lycopersico	662	8	16.3	8	2	Q76415_9SPER	Q76415 cycas taicu
590	8	16.3	7	2	P82445_TOBAC	P82445 nicotiana t	663	8	16.3	8	2	Q7M1F1_RAPSA	Q7M1F1 raphanus sa
591	8	16.3	7	2	Q8K3H6_RAT	Q8K3H6 rattus norv	664	8	16.3	8	2	Q8GTG5_LYCES	Q8GTG5 lycopersico
592	8	16.3	7	2	Q42564_FUGRU	Q42564 figu rubrip	665	8	16.3	8	2	Q9GCZ4_9LILI	Q9GCZ4 nenga pumil
593	8	16.3	7	2	Q99182_9SMEG	Q99182 gnatholebia	666	8	16.3	8	2	Q9GD47_9LILI	Q9GD47 hydrastelle
594	8	16.3	8	1	AKH_GROST	P84241 geotrupes s	667	8	16.3	8	2	Q9STD5_9ROSI	Q9STD5 begonia pal
595	8	16.3	8	1	AKH_MELML	P84240 melolontha	668	8	16.3	8	2	Q9T2Y1_9ROSI	Q9T2Y1 begonia apt
596	8	16.3	8	1	AKH_PACMA	P84242 pachnoda ma	669	8	16.3	8	2	Q9T2Y2_9ROSI	Q9T2Y2 begonia tai
597	8	16.3	8	1	COX6B_RAT	P80430 rattus norv	670	8	16.3	8	2	Q9T2Y3_9ROSI	Q9T2Y3 begonia for
598	8	16.3	8	1	HTF1_BLAOR	P84261 blatta orie	671	8	16.3	8	2	Q9TMN4_9ROSI	Q9TMN4 begonia for
599	8	16.3	8	1	HTF1_LEPDE	P84260 leptinotars	672	8	16.3	8	2	Q9XGL8_9ROSI	Q9XGL8 begonia chi
600	8	16.3	8	1	HTF1_PERAM	P84259 periplaneta	673	8	16.3	8	2	Q9XGL9_9ROSI	Q9XGL9 begonia nan
601	8	16.3	8	1	HTF_TENMO	P67789 tenebrio mo	674	8	16.3	8	2	Q79CX6_MYXXA	Q79CX6 myxococcus
602	8	16.3	8	1	HTF_ZOPRU	P67789 zophobas ru	675	8	16.3	8	2	Q7BW19_VIBCH	Q7BW19 vibrio chol
603	8	16.3	8	1	RECH_PANBO	P67939 pandalus bo	676	8	16.3	8	2	Q7M194_ECOLI	Q7M194 escherichia
604	8	16.3	8	1	UH09_RAT	P56575 rattus norv	677	8	16.3	8	2	Q8KXP4_9CHRO	Q8KXP4 microcystis
605	8	16.3	8	2	Q35752_YEAST	P56575 saccharomyc	678	8	16.3	8	2	Q8RJ10_STRCS	Q8RJ10 streptomyces
606	8	16.3	8	2	Q15893_HUMAN	Q15893 homo sapien	679	8	16.3	8	2	Q9AGP4_9NICC	Q9AGP4 arthrobacte
607	8	16.3	8	2	Q35900_HUMAN	Q35900 homo sapien	680	8	16.3	8	2	Q9X3K1_9PROC	Q9X3K1 prochloroco
608	8	16.3	8	2	Q95AE6_HUMAN	Q95AE6 homo sapien	681	8	16.3	8	2	Q60615_MOUSE	Q60615 mus musculu
609	8	16.3	8	2	Q5ZEY7_HUMAN	Q5ZEY7 homo sapien	682	8	16.3	8	2	Q7M039_RAT	Q7M039 rattus norv
610	8	16.3	8	2	Q9UMC7_HUMAN	Q9UMC7 homo sapien	683	8	16.3	8	2	Q7M056_9MURI	Q7M056 mus sp. gen
611	8	16.3	8	2	Q9Y4J4_HUMAN	Q9Y4J4 homo sapien	684	8	16.3	8	2	Q80WD6_MOUSE	Q80WD6 mus musculu
612	8	16.3	8	2	Q9Y4X6_HUMAN	Q9Y4X6 homo sapien	685	8	16.3	8	2	Q99NS0_AGOTA	Q99NS0 agouti tacz
613	8	16.3	8	2	Q6LDS6_HUMAN	Q6LDS6 homo sapien	686	8	16.3	8	2	Q99NS1_9HYST	Q99NS1 dinomys bra
614	8	16.3	8	2	Q53SB0_HUMAN	Q53SB0 homo sapien	687	8	16.3	8	2	Q99NS2_MYOCO	Q99NS2 myocaator c
615	8	16.3	8	2	Q548H6_HUMAN	Q548H6 homo sapien	688	8	16.3	8	2	Q99NS3_HYDHY	Q99NS3 hydrochoeru

689	8	16.3	8	2	Q9NS4_9HYST	Q9ns4	cavia tschu	762	8	16.3	9	2	Q9SDS6_9MAGN	Q9SDS6	magnolia wi
690	8	16.3	8	2	Q9NS5_DIPHE	Q9ns5	dipodomys h	763	8	16.3	9	2	Q9SDS7_9MAGN	Q9SDS7	magnolia si
691	8	16.3	8	2	Q9NS6_EREDO	Q9ns6	eredozia d	764	8	16.3	9	2	Q9SDT3_9MAGN	Q9SDT3	magnolia il
692	8	16.3	8	2	Q9NS7_CRIGR	Q9ns7	cricetus	765	8	16.3	9	2	Q9GCV6_9LILI	Q9GCV6	scleroperem
693	8	16.3	8	2	Q9NS8_RAT	Q9ns8	rattus norv	766	8	16.3	9	2	Q9GDI2_9LILI	Q9GDI2	linospadix
694	8	16.3	8	2	Q9NS9_MOUSE	Q9ns9	rattus musculu	767	8	16.3	9	2	Q9T3P3_MAGVI	Q9T3P3	magnolia vi
695	8	16.3	8	2	Q9NT0_PEDCA	Q9nt0	pedetes cap	768	8	16.3	9	2	Q9T3P4_MAGMA	Q9T3P4	magnolia ma
696	8	16.3	8	2	Q9NT1_CASCN	Q9nt1	castor cana	769	8	16.3	9	2	Q9THL5_9MAGN	Q9THL5	magnolia li
697	8	16.3	8	2	Q9NT2_TAMST	Q9nt2	tamias stri	770	8	16.3	9	2	Q9THL6_9MAGN	Q9THL6	magnolia si
698	8	16.3	8	2	Q6LD23_MOUSE	Q6ld23	mus musculu	771	8	16.3	9	2	Q9THL7_9MAGN	Q9THL7	magnolia si
699	8	16.3	8	2	Q9WJ33_9ALPH	Q9wj33	suid herpes	772	8	16.3	9	2	Q9THL8_9MAGN	Q9THL8	magnolia of
700	8	16.3	8	2	Q8QGN4_MEHV1	Q8qgn4	meleagrid h	773	8	16.3	9	2	Q9THL9_MAGPY	Q9THL9	magnolia py
701	8	16.3	8	2	P79940_XENLA	P79940	xenopus lae	774	8	16.3	9	2	Q9TMO_9MAGN	Q9TMO	magnolia fr
702	8	16.3	8	2	Q94V82_9SAUR	Q94v82	varanus yow	775	8	16.3	9	2	Q9TND7_LIRTU	Q9TND7	lirodendro
703	8	16.3	8	2	DNF1_LOCMI	P16339	locusta mig	776	8	16.3	9	2	Q9TND8_LIRCHI	Q9TND8	liriiodendro
704	8	16.3	9	1	FAR3_CALVO	P41858	calliphora	777	8	16.3	9	2	Q9TND9_MICFI	Q9TND9	melichia fi
705	8	16.3	8	1	FAR5_ASCSU	P43170	ascaris suu	778	8	16.3	9	2	Q9TNE0_9MAGN	Q9TNE0	melichia co
706	8	16.3	8	1	FAR9_ASCSU	P43172	ascaris suu	779	8	16.3	9	2	Q9TNE1_MAGLI	Q9TNE1	magnolia li
707	8	16.3	8	1	FARP_CALSI	P38495	callinectes	780	8	16.3	9	2	Q9TNE2_MAGAC	Q9TNE2	magnolia ac
708	8	16.3	8	1	FIBB_PAPHA	P13343	papio hamad	781	8	16.3	9	2	Q9TNE3_MAGST	Q9TNE3	magnolia st
709	8	16.3	8	1	LITO_LITAU	P08945	litorea aur	782	8	16.3	9	2	Q9TNE4_MAGSL	Q9TNE4	magnolia sa
710	8	16.3	8	1	LITR_PHYRO	P08946	phyllomedus	783	8	16.3	9	2	Q9TNE5_9MAGN	Q9TNE5	magnolia ko
711	8	16.3	8	1	MOSH_GLYJA	P19852	chylpeaster	784	8	16.3	9	2	Q9TNE6_9MAGN	Q9TNE6	magnolia de
712	8	16.3	8	1	NSK1_SARBU	P41492	sarcophaga	785	8	16.3	9	2	Q9TNE7_9MAGN	Q9TNE7	magnolia ni
713	8	16.3	8	1	UTAD_HUMAN	P31929	homo sapien	786	8	16.3	9	2	Q9TNE8_9MAGN	Q9TNE8	magnolia de
714	8	16.3	8	1	UPA3_HUMAN	P30089	homo sapien	787	8	16.3	9	2	Q9TNE9_9MAGN	Q9TNE9	magnolia co
715	8	16.3	8	2	Q5ILX3_MAGGR	Q5ilx3	magnaporthe	788	8	16.3	9	2	Q9TNF0_MAGTR	Q9TNF0	magnolia tr
716	8	16.3	8	2	Q14277_HUMAN	Q14277	homo sapien	789	8	16.3	9	2	Q9TNF1_9MAGN	Q9TNF1	magnolia he
717	8	16.3	8	2	Q16220_HUMAN	Q16220	homo sapien	790	8	16.3	9	2	Q9TNF2_9MAGN	Q9TNF2	magnolia ta
718	8	16.3	8	2	Q6LEH2_HUMAN	Q6leh2	homo sapien	791	8	16.3	9	2	Q9TNF3_9MAGN	Q9TNF3	magnolia sh
719	8	16.3	8	2	Q6LEK1_HUMAN	Q6lek1	homo sapien	792	8	16.3	9	2	Q9TNF4_9MAGN	Q9TNF4	magnolia sc
720	8	16.3	8	2	Q99887_HUMAN	Q99887	homo sapien	793	8	16.3	9	2	Q9TNF5_9MAGN	Q9TNF5	magnolia sc
721	8	16.3	8	2	Q9NYH5_HUMAN	Q9nyh5	homo sapien	794	8	16.3	9	2	Q9TNF6_MAGGA	Q9TNF6	magnolia gr
722	8	16.3	8	2	Q7M3N6_GRYBI	Q7m3n6	gryllus bim	795	8	16.3	9	2	Q4U0F2_MALDO	Q4U0F2	malus domes
723	8	16.3	8	2	Q7RHC2_PLAYO	Q7rhc2	plasmodium	796	8	16.3	9	2	Q45533_BACSU	Q45533	bacillus su
724	8	16.3	8	2	Q7RSP2_PLAYO	Q7rsp2	plasmodium	797	8	16.3	9	2	P83157_ANASU	P83157	anabaena sp
725	8	16.3	8	2	Q8W8X4_9SCHN	Q8w8x4	diadema mex	798	8	16.3	9	2	Q6LDL7_STAAL	Q6LDL7	staphylococ
726	8	16.3	8	2	Q4Y590_PLACH	Q4y590	plasmodium	799	8	16.3	9	2	Q712A6_SINSB	Q712A6	sinorhizobi
727	8	16.3	8	2	Q8HZY2_CANFA	Q8hzy2	canis famli	800	8	16.3	9	2	Q563E0_9CYAN	Q563E0	uncultured
728	8	16.3	8	2	Q8MJN1_CEBPY	Q8mjn1	cebuella py	801	8	16.3	9	2	Q35953_MOUSE	Q35953	mus musculu
729	8	16.3	8	2	Q8MJN2_CALJA	Q8mjn2	callithrix	802	8	16.3	9	2	Q7M078_RAT	Q7M078	rattus norv
730	8	16.3	8	2	Q8MJN3_CALGO	Q8mjn3	callimico g	803	8	16.3	9	2	Q8R514_RAT	Q8R514	rattus norv
731	8	16.3	8	2	Q8MJN4_LEORO	Q8mjn4	leontopithe	804	8	16.3	9	2	Q99MG3_MOUSE	Q99MG3	mus musculu
732	8	16.3	8	2	Q8MJN5_SAGFU	Q8mjn5	seguinus fu	805	8	16.3	9	2	Q9QWTO_MOUSE	Q9QWTO	mus musculu
733	8	16.3	8	2	Q8MJN6_AOTAZ	Q8mjn6	aotus azara	806	8	16.3	9	2	Q62530_MUSSP	Q62530	mus spretus
734	8	16.3	8	2	Q8MJN7_SAISS	Q8mjn7	saimiri sci	807	8	16.3	9	2	Q71067_9PARA	Q71067	canine diet
735	8	16.3	8	2	Q8MJN8_CEBAP	Q8mjn8	cebus apell	808	8	16.3	9	2	Q71068_9PARA	Q71068	canine diet
736	8	16.3	8	2	Q8MJN9_ATEFU	Q8mjn9	ateles fuec	809	8	16.3	9	2	Q83622_9FLAV	Q83622	murray vall
737	8	16.3	8	2	Q9PT77_BOVIN	Q9pt77	bos taurus	810	8	16.3	9	2	Q7LZ66_MELGA	Q7LZ66	meleagris g
738	8	16.3	8	2	Q9XSL0_CAPHI	Q9xsl0	capra hircu	811	8	16.3	9	2	Q7LZ75_RANES	Q7LZ75	rana esculu
739	8	16.3	8	2	Q6JDL5_CANFA	Q6jdl5	canis famli	812	8	16.3	9	2	Q94V10_VARGI	Q94V10	varanus g9
740	8	16.3	8	2	Q6LAP2_SMIMA	Q6lap2	sminthopsis	813	8	16.3	9	2	Q16047_HUMAN	Q16047	homo sapien
741	8	16.3	8	2	Q5D4Y6_9MYRT	Q5d4y6	capuronia m	814	7	14.3	4	1	FLRN_ATEL	FLRN	anthopleura
742	8	16.3	8	2	Q5EFY1_9BRYTO	Q5efy1	polytrichum	815	7	14.3	5	1	PAP2_PARMA	PAP2	parma
743	8	16.3	8	2	Q5VH65_9ASPA	Q5vh65	hymenocalli	816	7	14.3	5	1	PRCT_CARMA	PRCT	carma
744	8	16.3	8	2	Q5VH71_9ASPA	Q5vh71	chlidanthus	817	7	14.3	5	1	PRCT_CARMA	PRCT	carma
745	8	16.3	8	2	Q6EX64_9LAMI	Q6ex64	hyptis flor	818	7	14.3	5	1	PRCT_LIMPO	PRCT	limpus pol
746	8	16.3	8	2	Q6PT73_ZIZANIA	Q6pt73	zizania aqu	819	7	14.3	5	1	PRCT_PERAM	PRCT	periphaneca
747	8	16.3	8	2	Q6PT74_9FOAL	Q6pt74	streptochaee	820	7	14.3	5	1	OVN_LEPDE	OVN	leptinotars
748	8	16.3	8	2	Q6PT75_SORBI	Q6pt75	sorghum bic	821	7	14.3	7	1	ALL3_CARMA	ALL3	carcinus ma
749	8	16.3	8	2	Q6PT76_LOLPR	Q6pt76	lolium pere	822	7	14.3	7	1	ALL4_CARMA	ALL4	carcinus ma
750	8	16.3	8	2	Q6PT77_DANSP	Q6pt77	danthonia s	823	7	14.3	7	1	ALL5_CARMA	ALL5	carcinus ma
751	8	16.3	8	2	Q6PT78_9FOAL	Q6pt78	chasmantanthu	824	7	14.3	7	1	DEM_PHYHY	DEM	phyllomedus
752	8	16.3	8	2	Q6PT79_9FOAL	Q6pt79	bouteloua g	825	7	14.3	7	1	FAR1_HELFI	FAR1	helisoma tr
753	8	16.3	8	2	Q7X6A3_MAIZE	Q7x6a3	zea mays (m	826	7	14.3	7	1	FAR4_PANRE	FAR4	panagrellus
754	8	16.3	8	2	Q8MEM3_9ROSI	Q8mem3	howittia tr	827	7	14.3	7	1	FARB_CALVO	FARB	calliphora
755	8	16.3	8	2	Q95DR8_9MAGN	Q95dr8	michellia ma	828	7	14.3	7	1	UN06_PINS	UN06	pinus pinas
756	8	16.3	8	2	Q95DR9_9MAGN	Q95dr9	manglietia	829	7	14.3	7	2	Q8NH77_HUMAN	Q8NH77	homo sapien
757	8	16.3	8	2	Q95DS0_9MAGN	Q95ds0	manglietia	830	7	14.3	7	2	Q66113_9COMO	Q66113	cherry leaf
758	8	16.3	8	2	Q95DS1_9MAGN	Q95ds1	manglietia	831	7	14.3	7	2	Q8UJ20_CHICK	Q8UJ20	gallus gall
759	8	16.3	8	2	Q95DS2_9MAGN	Q95ds2	magnolia ov	832	7	14.3	8	1	AKH_LITAU	AKH	libellula a
760	8	16.3	8	2	Q95DS4_9MAGN	Q95ds4	magnolia do	833	7	14.3	8	1	ALL16_CARMA	ALL16	carcinus ma
761	8	16.3	8	2	Q95DS5_9MAGN	Q95ds5	magnolia sa	834	7	14.3	8	1	ALL13_CYPDO	ALL13	cydia pomon

835	7	14.3	8	1	ALL4 CALVO	P41840 calliphora	908	7	14.3	9	1	CX6A1 THOOB	P80975 thunnus obe
836	7	14.3	8	1	ALL9 CARMA	P81812 carcinus ma	909	7	14.3	9	1	FAR1 CALVO	P41856 calliphora
837	7	14.3	8	1	COM2 CONFU	P58785 conus purpu	910	7	14.3	9	1	FAR2 CALVO	P41857 calliphora
838	7	14.3	8	1	LCK1 PANRE	P41872 panagrellus	911	7	14.3	9	1	FAR4 CALVO	P41859 calliphora
839	7	14.3	8	1	LCK2 LEUMA	P21141 leucophaea	912	7	14.3	9	1	FAR4 PENNO	P83319 penaeus mon
840	7	14.3	8	1	LCK7 LEUMA	P19989 leucophaea	913	7	14.3	9	1	FAR5 PANRE	P84861 panagrellus
841	7	14.3	8	1	LMT2 LOEMI	P22396 locusta mig	914	7	14.3	9	1	FAR5 PENNO	P83320 penaeus mon
842	7	14.3	8	1	NMBB BOVIN	P82618 periplaneta	915	7	14.3	9	1	FARA CALVO	P41865 calliphora
843	7	14.3	8	1	PPK3 PERAM	P30096 homo sapien	916	7	14.3	9	1	FNRF1 SARBU	P83350 sarcophaga
844	7	14.3	8	1	UPA10 HUMAN	P74404 aspergillus	917	7	14.3	9	1	LMT3 LOEMI	P41489 locusta mig
845	7	14.3	8	2	Q7MAU4 ASPFI	Q74404 aspergillus	918	7	14.3	9	1	NEUU CAVPO	P34966 cavia porce
846	7	14.3	8	2	Q15888 HUMAN	Q15888 homo sapien	919	7	14.3	9	1	PWK2 SARBU	P84353 sarcophaga
847	7	14.3	8	2	Q15901 HUMAN	Q15901 homo sapien	920	7	14.3	9	1	PYF2 PENNO	P84006 penaeus mon
848	7	14.3	8	2	Q6BC29 HUMAN	Q6bc29 homo sapien	921	7	14.3	9	1	PYF3 PENNO	P84007 penaeus mon
849	7	14.3	8	2	Q6LC12 HUMAN	Q6lc12 homo sapien	922	7	14.3	9	1	RS10 SERNA	O69936 serratia ma
850	7	14.3	8	2	Q71UR9 HUMAN	Q71ur9 homo sapien	923	7	14.3	9	1	SAMP MUSCA	P19095 mustelus ca
851	7	14.3	8	2	Q7KYV5 HUMAN	Q7kyv5 homo sapien	924	7	14.3	9	1	SAP SNOVA	P24047 stomopneute
852	7	14.3	8	2	Q7Z7I9 HUMAN	Q7z7i9 homo sapien	925	7	14.3	9	1	TKLI LOEMI	P16223 locusta mig
853	7	14.3	8	2	Q81UB8 HUMAN	Q81ub8 homo sapien	926	7	14.3	9	1	UPA6 HUMAN	P30092 homo sapien
854	7	14.3	8	2	Q81VK3 HUMAN	Q81vk3 homo sapien	927	7	14.3	9	2	Q16386 HUMAN	P16386 homo sapien
855	7	14.3	8	2	Q9P0K3 HUMAN	Q9p0k3 homo sapien	928	7	14.3	9	2	Q5QEX9 HUMAN	Q5qex9 homo sapien
856	7	14.3	8	2	Q9UJ50 HUMAN	Q9uj50 homo sapien	929	7	14.3	9	2	Q67A08 HUMAN	Q67a08 homo sapien
857	7	14.3	8	2	Q9Y4J3 HUMAN	Q9y4j3 homo sapien	930	7	14.3	9	2	Q67AR5 HUMAN	Q67ar5 homo sapien
858	7	14.3	8	2	Q9HCQ3 HUMAN	Q9hcq3 homo sapien	931	7	14.3	9	2	Q67AT6 HUMAN	Q67at6 homo sapien
859	7	14.3	8	2	Q7M3S3 9TRYP	Q7m3s3 trypanosoma	932	7	14.3	9	2	Q6QF45 HUMAN	Q6qf45 homo sapien
860	7	14.3	8	2	Q94623 MANSE	Q94623 manduca sex	933	7	14.3	9	2	Q7KYP6 HUMAN	Q7kyp6 homo sapien
861	7	14.3	8	2	Q9TWH6 9ANNE	Q9twh6 perinereis	934	7	14.3	9	2	Q7M4Q9 HUMAN	Q7m4q9 homo sapien
862	7	14.3	8	2	Q7REE2 PLAYO	Q7ree2 plasmodium	935	7	14.3	9	2	Q8NHL3 HUMAN	Q8nhl3 homo sapien
863	7	14.3	8	2	Q7MAH6 9ODON	Q7mah6 ischnura se	936	7	14.3	9	2	Q9UCQ9 HUMAN	Q9ucq9 homo sapien
864	7	14.3	8	2	Q7MAH7 9ODON	Q7mah7 pseudogrion	937	7	14.3	9	2	Q14715 HUMAN	Q14715 homo sapien
865	7	14.3	8	2	Q18854 CANFA	Q18854 canis famli	938	7	14.3	9	2	Q15999 HUMAN	Q15999 homo sapien
866	7	14.3	8	2	Q9RLS9 FIG	Q9rls9 sus scrofa	939	7	14.3	9	2	Q9TWD6 LEPDE	Q9twd6 leptinotars
867	7	14.3	8	2	Q85U13 SECST	Q85u13 secale stri	940	7	14.3	9	2	Q7RA82 PLAYO	Q7ra82 plasmodium
868	7	14.3	8	2	Q85U18 PSAFR	Q85u18 psathyrosta	941	7	14.3	9	2	Q7RDA8 PLAYO	Q7rda8 plasmodium
869	7	14.3	8	2	Q85U43 9FOAL	Q85u49 australopyr	942	7	14.3	9	2	Q8WFT4 9ECHN	Q8wft4 diadema ant
870	7	14.3	8	2	Q5EX87 9LAMI	Q5ex87 streptocarp	943	7	14.3	9	2	Q4Y4I3 PLACH	Q4y4i3 plasmodium
871	7	14.3	8	2	Q5IA47 9WAGN	Q5ia47 laurus nobi	944	7	14.3	9	2	Q7M4D5 DIASE	Q7m4d5 diadema set
872	7	14.3	8	2	Q6EX61 9LAMI	Q6ex61 isodon hisp	945	7	14.3	9	2	Q28112 BOVIN	Q28112 bos taurus
873	7	14.3	8	2	Q6H0C6 9TRAC	Q6h0c6 isoetes fla	946	7	14.3	9	2	Q28121 BOVIN	Q28121 bos taurus
874	7	14.3	8	2	Q6YLT8 SCIVE	Q6ylt8 sciadopitys	947	7	14.3	9	2	Q5G6J7 CRATH	Q5g6j7 craseonycte
875	7	14.3	8	2	Q7IMR4 BRANA	Q7imr4 brassica na	948	7	14.3	9	2	Q5G6J8 9CHIR	Q5g6j8 eumops auri
876	7	14.3	8	2	Q7KES5 9MYRT	Q7kes5 leptospermu	949	7	14.3	9	2	Q5G6J9 NATST	Q5g6j9 natalus str
877	7	14.3	8	2	Q87471 HABIN	Q87471 haemophilus	950	7	14.3	9	2	Q5G6K5 9CHIR	Q5g6k5 rhogessa t
878	7	14.3	8	2	Q49534 MYCHO	Q49534 mycoplasma	951	7	14.3	9	2	Q6LDS7 RABIT	Q6lds7 oryctolagus
879	7	14.3	8	2	Q6LAA8 SHIFL	Q6laa8 shigella fl	952	7	14.3	9	2	Q6UI03 MACMU	Q6ui03 macaca mula
880	7	14.3	8	2	Q71UF7 MORMO	Q71uf7 morganella	953	7	14.3	9	2	Q7M2K6 RABIT	Q7m2k6 oryctolagus
881	7	14.3	8	2	Q799V9 BAGSH	Q799v9 bacillus sp	954	7	14.3	9	2	Q7M2M7 BOVIN	Q7m2m7 bos taurus
882	7	14.3	8	2	Q8GL21 BORBU	Q8gl21 borrelia bu	955	7	14.3	9	2	Q7M2N8 BOVIN	Q7m2n8 bos indicus
883	7	14.3	8	2	Q9R7T2 ECOLI	Q9r7t2 escherichia	956	7	14.3	9	2	Q7M375 BOVIN	Q7m375 bos taurus
884	7	14.3	8	2	Q9ZIE9 NEIME	Q9zie9 neisseria m	957	7	14.3	9	2	Q7M394 FIG	Q7m394 sus scrofa
885	7	14.3	8	2	Q7M124 KLUCI	Q7m124 kluyvera ci	958	7	14.3	9	2	Q5IA45 MAHBE	Q5ia45 mahonia bea
886	7	14.3	8	2	Q79AG6 ENTAG	Q79ag6 enterobacte	959	7	14.3	9	2	Q6VR25 THECC	Q6vr25 theobroma c
887	7	14.3	8	2	Q99NX3 HYDHY	Q99nx3 hydrochoeru	960	7	14.3	9	2	Q7OY83 9LAMI	Q7oy83 plectranthu
888	7	14.3	8	2	Q99P40 MOUSE	Q99p40 mus musculu	961	7	14.3	9	2	Q7EXP6 HORVD	Q7exp6 hordium vul
889	7	14.3	8	2	Q9ET16 MESAU	Q9et16 meocricetu	962	7	14.3	9	2	Q8MBF4 IPOQU	Q8mbf4 ipomoea qua
890	7	14.3	8	2	Q9ET17 MUSCR	Q9et17 mus caroli	963	7	14.3	9	2	Q8VZZ3 PINRA	Q8vzz3 pinus radia
891	7	14.3	8	2	Q9ET18 MUSSP	Q9et18 mus spretus	964	7	14.3	9	2	Q9FEC0 HORVU	Q9fec0 hordium vul
892	7	14.3	8	2	Q9QV15 9MURI	Q9qv15 rattus sp.	965	7	14.3	9	2	Q9TKD9 9MYRT	Q9tkd9 pericalymma
893	7	14.3	8	2	Q9QVJ8 9MURI	Q9qvj8 mus sp. nep	966	7	14.3	9	2	Q9TKF2 9MYRT	Q9tkf2 asteromyrca
894	7	14.3	8	2	Q78ED1 RAT	Q78ed1 rattus norv	967	7	14.3	9	2	Q9TKG1 9MYRT	Q9tkg1 calothamius
895	7	14.3	8	2	Q62528 MUSSP	Q62528 mus spretus	968	7	14.3	9	2	Q5SBX0 9FOAL	Q5sbx0 reatio inei
896	7	14.3	8	2	Q56T42 9GEMI	Q56t42 okra yellow	969	7	14.3	9	2	Q4QWV3 9MARC	Q4qvw3 pallavicini
897	7	14.3	8	2	Q83349 9CORO	Q83349 murine hepa	970	7	14.3	9	2	Q4QWV9 9MARC	Q4qvw9 jensenia sp
898	7	14.3	8	2	Q5YDW3 9PERC	Q5ydw3 xiphister m	971	7	14.3	9	2	Q48686 LACLC	Q48686 lactococcus
899	7	14.3	8	2	Q6UTU8 ONCMY	Q6utu8 oncorhynch	972	7	14.3	9	2	P83539 LACSN	P83539 lactobacill
900	7	14.3	8	2	Q6UA69 CARCW	Q6ua69 carassius c	973	7	14.3	9	2	Q673B1 9CHLR	Q673b1 dehalococo
901	7	14.3	8	2	Q7LZ21 CHICK	Q7lzz21 gallus gall	974	7	14.3	9	2	Q6Q7P3 ALCEU	Q6q7p3 alcaligenes
902	7	14.3	8	2	Q7LZ46 CTEID	Q7lzz46 ctenopharyn	975	7	14.3	9	2	Q6VCX0 9ACTO	Q6vcx0 streptomyce
903	7	14.3	8	2	Q7T282 9GRONI	Q7t282 geochelone	976	7	14.3	9	2	Q71UF6 YEREN	Q71uf6 versinia en
904	7	14.3	8	2	Q8J3J5 9PASS	Q8jj35 ficedula hy	977	7	14.3	9	2	Q7M151 9BACT	Q7m151 unidentified
905	7	14.3	8	2	Q7LZ27 NAJOX	Q7lzz27 najia oxiana	978	7	14.3	9	2	Q8GLJ1 BORBU	Q8glj1 borrelia bu
906	7	14.3	9	1	BUK CLOPA	P81337 clostridium	979	7	14.3	9	2	Q51765 PSEFL	Q51765 pseudomonas
907	7	14.3	9	1	COW CONVE	P83047 conus ventr	980	7	14.3	9	2	Q6YF34 RAT	Q6yf34 rattus norv

981 7 14.3 9 2 Q80X07 mus sp. chr
 982 7 14.3 9 2 Q80Y66 mus musculus
 983 7 14.3 9 2 Q8CG13 mouse
 984 7 14.3 9 2 Q4W8Q9 mouse
 985 7 14.3 9 2 Q9QZAB mouse
 986 7 14.3 9 2 Q65711 BEV
 987 7 14.3 9 2 Q66545 human herpe
 988 7 14.3 9 2 Q67605 squash leaf
 989 7 14.3 9 2 Q67606 squash leaf
 990 7 14.3 9 2 Q84333 simian viru
 991 7 14.3 9 2 Q8QVD3 ovine respi
 992 7 14.3 9 2 Q88612 middelburg
 993 7 14.3 9 2 Q31653 anser caeru
 994 7 14.3 9 2 Q5YDV1 xiphister m
 995 7 14.3 9 2 Q673X9 malacodonut
 996 7 14.3 9 2 Q6Q790 rana ridibu
 997 7 14.3 9 2 Q7SX77 geochelone
 998 7 14.3 9 2 Q8AUM7 carassius a
 999 7 14.3 9 2 Q8AYL5 carassius a
 1000 7 14.3 9 2 Q8UTD7 human immun

ALIGNMENTS

RESULT 1
 Q05403 YEAST
 ID Q05403_YEAST PRELIMINARY; PRT; 8 AA.
 AC Q05403;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Orf 00915 protein (Fragment).
 GN Name=orf 00915;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FY1679;
 RX MEDLINE=96021609; PubMed=8533473;
 RA Zumeitein E., Pearson B.M., Kalogeropoulos A., Schweitzer M.;
 RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
 RT more than twice as many unknown as known open reading frames.";
 RL Yeast 11:975-986(1995).
 DR EMBL; X83121; CAA58183.1; -; Genomic_DNA.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 42.9%; Score 21; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 HNV 9
 Db :|||
 2 HNV 5

RESULT 2
 FUSS FUSSO
 ID FUSS FUSSO STANDARD; PRT; 8 AA.
 AC P81010;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Allergen Fus s i3596* (Fragment).
 OS Fusarium solani subsp. pisi (Nectria haematococca)
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocerales; Nectriaceae; Nectria.
 OX NCBI_TaxID=70791;
 RN [1]
 RP PROTEIN SEQUENCE.

RC STRAIN=IARI 3596; TISSUE=Mycelium;
 RA Verma J., Gangal S.V.;
 RL Submitted (JUL-1997) to Swiss-Prot.
 CC -!- ALLERGEN: Causes an allergic reaction in human.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
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KW Allergen; Direct protein sequencing.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 36.7%; Score 18; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 HNV 9
 Db :|||
 5 HNV 7

RESULT 3
 Q4VS04 MANSE
 ID Q4VS04_MANSE PRELIMINARY; PRT; 8 AA.
 AC Q4VS04;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Calcium-activated potassium channel alpha subunit (Fragment).
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm)
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Megoptera; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
 OC Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Keyser M.R., Witten J.L.;
 RT "Calcium-Activated Potassium Channel of the Tobacco Hornworm Manduca
 RT sexta: Molecular Characterization and Expression Analysis.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY644788; AAT44362.1; -; mRNA.
 KW Ionic channel.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 785 MW; 80A1B771AAB7776D CRC64;

Query Match 36.7%; Score 18; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 APP 5
 Db :|||
 1 APP 3

RESULT 4
 Q9J205 9HEPC
 ID Q9J205_9HEPC PRELIMINARY; PRT; 8 AA.
 AC Q9J205;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Truncated polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HC41;

```

RX MEDLINE=22089303; PubMed=12094871;
RA Fan X., Di Bisceglie A.M.;
RT "Genetic complexity and serum reactivity of HVR1 quasispecies of
RT hepatitis C virus in patients with cirrhosis.";
RL Am. J. Gastroenterol. 97:1489-1495(2002).
DR EMBL: AF211054; AAF30114.1; -; Genomic_DNA.
KW Polypeptide.
FT NON_TER
SQ SEQUENCE 8 AA; 917 MW; B1D41AFAP7776DCA CRC64;

Query Match 36.7%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APP 5
DB 2 APP 4

RESULT 5
YBFR_AZOV1
ID YBFR_AZOV1 STANDARD; PRT; 9 AA.
AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical protein in bfr 3'region (Fragment).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=92196129; PubMed=1549605;
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RA Stiefel E.I.;
RT "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
DR EMBL: M83692; AAA22122.1; -; Genomic_DNA.
DR PIR: B41983; B41983.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B417776D CRC64;

Query Match 36.7%; Score 18; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APP 5
DB 2 APP 4

RESULT 6
Q6SP94_CHLRE
ID Q6SP94_CHLRE PRELIMINARY; PRT; 9 AA.
AC Q6SP94_
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE PF26 (Fragment).
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
OC Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CC-2290;
RX MEDLINE=22570934; PubMed=12684385; DOI=10.1128/EC.2.2.362-379.2003;
RA Kathir P., LaVoie M., Brazelton W.J., Haas N.A., Lefebvre P.A.,
RA Silflow C.D.;
RT "Molecular map of the Chlamydomonas reinhardtii nuclear genome.";
RL Eukaryot. Cell 2:362-379(2003).
DR EMBL: AY454155; AAR20844.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 9 AA; 1012 MW; DB0AAB1B1B0776D CRC64;

Query Match 36.7%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APP 5
DB 2 APP 4

RESULT 7
Q99193_PSEPU
ID Q99193_PSEPU PRELIMINARY; PRT; 9 AA.
AC Q99193;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE RPOB beta-subunit of RNA polymerase (Fragment).
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Borodin A.M., Danilkovich A.V., Allikmets R.L., Rostapshov V.M.,
RA Chernov I.P., Azhikina T.L., Monastyrskaya S., Sverdlov D.;
RT "Nucleotide sequence of the rpoB gene coding for the beta-subunit of
RT RNA polymerase in Pseudomonas putida.";
RL Dokl. Biochem. 302:1261-1265(1988).
DR EMBL: X15849; CAA33847.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 9 AA; 852 MW; 5B4167776DC76727 CRC64;

Query Match 36.7%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APP 5
DB 5 APP 7

RESULT 8
Q84U84_SOYBN
ID Q84U84_SOYBN PRELIMINARY; PRT; 9 AA.
AC Q84U84;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Flavonoid 3'-hydroxylase (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22474238; PubMed=12586717;
RA Zabala G., Vodkin L.;
RT "Cloning of the pleiotropic T locus in soybean and two recessive
RT alleles that differentially affect structure and expression of the
RT encoded flavonoid 3' hydroxylase.";
RL Genetics 163:295-309(2003).

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DR EMBL; AF499732; AAO47848.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 9 AA; 978 MW; 25A0B685AB42C1F7 CRC64;

Query Match      34.7%; Score 17; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.2e+06;
Matches 3; Conservative 3; Mismatches 0; Gaps 0;

QY 3 APPVHNV 9
   ||| |:::
DB 1 APHVYSM 7

RESULT 9
ALL6_CVDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cydastatin-6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829; DOI=10.1016/S0196-9781(97)00188-5;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the allatostatin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 8
   ||| |:::
FT SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match      32.7%; Score 16; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 2; Mismatches 0; Gaps 0;

QY 5 PVHNV 8
   ||| |:::
DB 2 PLYN 5

RESULT 10
Q6Y2F2_CITSI
ID Q6Y2F2_CITSI PRELIMINARY; PRT; 8 AA.
AC Q6Y2F2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Vacuolar invertase (Fragment).
OS Citrus sinensis (Sweet orange).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosida II; Sapindales; Rutaceae; Citrus.
OX NCBI_TaxID=2711;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA An X., Zhang S., Xu C., Qin Q.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AY190016; AAO73818.1; -; Genomic_DNA.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1013 MW; FE21E1FB4771AAA6 CRC64;

Query Match      32.7%; Score 16; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 PVHNV 9
   ||| |:::
DB 4 PYHHL 8

RESULT 11
Q7M067_MOUSE
ID Q7M067_MOUSE PRELIMINARY; PRT; 8 AA.
AC Q7M067;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumor-associated antigen MUT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=94217811; PubMed=8164742; DOI=10.1038/369067a0;
RA Mandelboim O., Berke G., Fridkin M., Feldman M., Eisenstein M.,
RA Eisenbach L.;
RT "CTL induction by a tumour-associated antigen octapeptide derived from
RT a murine lung carcinoma.";
RL Nature 369:67-71(1994).
DR PIR; S43971; S43971.
SQ SEQUENCE 8 AA; 934 MW; 9976DDC1A456DB19 CRC64;

Query Match      32.7%; Score 16; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STAPP 5
   ||| |
DB 4 NTAQP 8

RESULT 12
Q9P8E5_KLJULA
ID Q9P8E5_KLJULA PRELIMINARY; PRT; 9 AA.
AC Q9P8E5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HIS4 protein (Fragment).
OS Name=HIS4;
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NRRL-Y1140;
RX MEDLINE=99449382; PubMed=10518937; DOI=10.1016/S0014-5793(99)01105-9;
RA Lamas-Maceiras M., Esperanza Cerdan E., Freire-Picos M.A.;
RT "Kluyveromyces lactis HIS4 transcriptional regulation: similarities
RT and differences to Saccharomyces cerevisiae HIS4 gene.";
RL FEBS Lett. 458:72-76(1999).
DR EMBL; AJ238494; CAB87125.1; -; Genomic_DNA.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

Query Match      32.7%; Score 16; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
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Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 PVHN 8
Db 6 PVFN 9

RESULT 13
Q71UR3 HUMAN
ID Q71UR3 HUMAN PRELIMINARY; PRT; 9 AA.
AC Q71UR3;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Collagen type XII alpha 1 (Fragment).
GN Name=COL12A1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99041554; PubMed=9826181;
RA Chiquet M., Mumenthaler U., Wittwer M., Jin W., Koch M.;
RT "The chick and human collagen alpha1(XII) gene promoter. activity of
RT highly conserved regions around the first exon and in the first
RT intron.";
RL Bur. J. Biochem. 257:362-371(1998).
DR EMBL, AF061871; AAC83578.1; -; Genomic_DNA.
KW Collagen.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1040 MW; 6214C77673415A4 CRC64;

Query Match 32.7%; Score 16; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 STAPP 5
Db 3 SFLPP 7

RESULT 14
Q72ZE2 HUMAN
ID Q72ZE2 HUMAN PRELIMINARY; PRT; 9 AA.
AC Q72ZE2;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DE RPS6KA3 protein (Fragment).
GN Name=RPS6KA3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
RA Kitano T., Schwarz C., Nickel B., Paabo S.;
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and
RT chimpanzees.";
RL Mol. Biol. Evol. 20:1281-1289(2003).
DR EMBL, AB102341; BAC80840.1; -; Genomic_DNA.
DR EMBL, AB102342; BAC80841.1; -; Genomic_DNA.
DR EMBL, AB102343; BAC80842.1; -; Genomic_DNA.
DR EMBL, AB102344; BAC80843.1; -; Genomic_DNA.
DR EMBL, AB102345; BAC80844.1; -; Genomic_DNA.
DR EMBL, AB102346; BAC80845.1; -; Genomic_DNA.
DR EMBL, AB102347; BAC80846.1; -; Genomic_DNA.
DR EMBL, AB102348; BAC80847.1; -; Genomic_DNA.
DR EMBL, AB102349; BAC80848.1; -; Genomic_DNA.

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DR EMBL, AB102350; BAC80849.1; -; Genomic_DNA.
DR EMBL, AB102351; BAC80850.1; -; Genomic_DNA.
DR EMBL, AB102352; BAC80851.1; -; Genomic_DNA.
DR EMBL, AB102353; BAC80852.1; -; Genomic_DNA.
DR EMBL, AB102354; BAC80853.1; -; Genomic_DNA.
DR EMBL, AB102355; BAC80854.1; -; Genomic_DNA.
DR EMBL, AB102356; BAC80855.1; -; Genomic_DNA.
DR EMBL, AB102357; BAC80856.1; -; Genomic_DNA.
DR EMBL, AB102358; BAC80857.1; -; Genomic_DNA.
DR EMBL, AB102359; BAC80858.1; -; Genomic_DNA.
DR EMBL, AB102360; BAC80859.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 939 MW; D8C6C045B1F2C862 CRC64;

Query Match 32.7%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 6 VHNV 9
Db 4 VHSI 7

RESULT 15
Q7YQC2 PANTR
ID Q7YQC2 PANTR PRELIMINARY; PRT; 9 AA.
AC Q7YQC2;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DE RPS6KA3 protein (Fragment).
GN Name=RPS6KA3;
OS Pan troglodytes verus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=37012;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
RA Kitano T., Schwarz C., Nickel B., Paabo S.;
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and
RT chimpanzees.";
RL Mol. Biol. Evol. 20:1281-1289(2003).
DR EMBL, AB102361; BAC80860.1; -; Genomic_DNA.
DR EMBL, AB102362; BAC80861.1; -; Genomic_DNA.
DR EMBL, AB102363; BAC80862.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 939 MW; D8C6C045B1F2C862 CRC64;

Query Match 32.7%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 6 VHNV 9
Db 4 VHSI 7

RESULT 16
Q7YQC3 PANTR
ID Q7YQC3 PANTR PRELIMINARY; PRT; 9 AA.
AC Q7YQC3;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DE RPS6KA3 protein (Fragment).
GN Name=RPS6KA3;
OS Pan troglodytes troglodytes.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

```

OC Pan.
OX NCBI_TaxID=37011;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22763540; PubMed=12777533; DOI=10.1093/molbev/msg134;
RA Kitano T., Schwarz C., Nickel B., Paabo S.;
RT "Gene diversity patterns at 10 X-chromosomal loci in humans and
chimpanzees";
RL Mol. Biol. Evol. 20:1281-1289(2003).
DR EMBL; AB102364; BAC80863.1; -; Genomic DNA.
DR EMBL; AB102365; BAC80864.1; -; Genomic DNA.
DR EMBL; AB102366; BAC80865.1; -; Genomic DNA.
DR EMBL; AB102367; BAC80866.1; -; Genomic DNA.
DR EMBL; AB102368; BAC80867.1; -; Genomic DNA.
DR EMBL; AB102369; BAC80868.1; -; Genomic DNA.
DR EMBL; AB102370; BAC80869.1; -; Genomic DNA.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 939 MW; D8C6C045B1P2C862 CRC64;

Query Match 32.7%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.2e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 VHNV 9
DB 4 VHSI 7

RESULT 17
Q76FUI_9FLOR PRELIMINARY; PRT; 9 AA.
AC Q76FUI;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE Rubisco large subunit (Fragment).
GN Name=rbcl;
OS Plocamium telfairiae.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Plocamiales; Plocamiaceae;
OC Plocamium.
OX NCBI_TaxID=38522;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yano T., Kamiya M., Arai S., Kawai H.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB104699; BAC82401.1; -; Genomic DNA.
DR EMBL; AB104702; BAC82407.1; -; Genomic DNA.
DR EMBL; AB104703; BAC82409.1; -; Genomic DNA.
DR EMBL; AB104705; BAC82413.1; -; Genomic DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 993 MW; CA1A55A1B771AB02 CRC64;

Query Match 32.7%; Score 16; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVHNV 9
DB 5 PTSNV 9

RESULT 18
Q76FUS_9FLOR PRELIMINARY; PRT; 9 AA.
AC Q76FUS;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Rubisco large subunit (Fragment).

GN Name=rbcl;
OS Plocamium serrulatum.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Plocamiales; Plocamiaceae;
OC Plocamium.
OX NCBI_TaxID=223160;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yano T., Kamiya M., Arai S., Kawai H.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB104697; BAC82397.1; -; Genomic DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 979 MW; CA1A55A1B771AB2 CRC64;

Query Match 32.7%; Score 16; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVHNV 9
DB 5 PTSNV 9

RESULT 19
Q76FU7_9FLOR PRELIMINARY; PRT; 9 AA.
AC Q76FU7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Rubisco large subunit (Fragment).
GN Name=rbcl;
OS Plocamium recurvatum.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Plocamiales; Plocamiaceae;
OC Plocamium.
OX NCBI_TaxID=223159;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yano T., Kamiya M., Arai S., Kawai H.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB104696; BAC82395.1; -; Genomic DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 993 MW; CA1A55A1B771AB02 CRC64;

Query Match 32.7%; Score 16; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVHNV 9
DB 5 PTSNV 9

RESULT 20
Q76FV1_9FLOR PRELIMINARY; PRT; 9 AA.
AC Q76FV1;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE Rubisco large subunit (Fragment).
GN Name=rbcl;
OS Plocamium ovicornis.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Plocamiales; Plocamiaceae;
OC Plocamium.
OX NCBI_TaxID=223158;
RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Yano T., Kamiya M., Arai S., Kawai H.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB104694; BAC82389.1; -; Genomic DNA.
 DR EMBL; AB104693; BAC82389.1; -; Genomic DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 979 MW; CA1A55A1B771AAB2 CRC64;
 Query Match 32.7%; Score 16; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 PVHNV 9
 DB 5 PTSNV 9

RESULT 21
 ID Q76FV7_PLOCA
 AC Q76FV7_PLOCA PRELIMINARY; PRT; 9 AA.
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
 DE Rubisco large subunit (Fragment).
 GN Name=rbcL;
 OS Plocamium cartilagineum (Red comb weed).
 OC Chloroplast.
 OC Eukaryota; Rhodophyta; Florideophyceae; Plocamiales; Plocamiaceae;
 OC Plocamium.
 OX NCBI_TaxID=31452;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Yano T., Kamiya M., Arai S., Kawai H.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB104691; BAC82385.1; -; Genomic DNA.
 DR EMBL; AB104692; BAC82387.1; -; Genomic DNA.
 DR EMBL; AB104690; BAC82383.1; -; Genomic DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 993 MW; CA1A55A1B771AAB02 CRC64;
 Query Match 32.7%; Score 16; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 PVHNV 9
 DB 5 PTSNV 9

RESULT 22
 ID Q64972_AVEVR
 AC Q64972_AVEVR PRELIMINARY; PRT; 9 AA.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Rous associated virus type 1 (RAV-1) ml protein, 3' end, and env protein (Fragment).
 DE Avian rous-associated virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
 OX NCBI_TaxID=11950;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=89037349; PubMed=2846875;
 RA Marx M., Criaenti P., Eychene A., Bechade C., Laugier D.,
 RA Ghyssels J., Pessac B., Calochy G.;
 RT "Activation and transduction of c-mil sequences in chicken neuroretina cells induced to proliferate by infection with avian lymphomatosis

RT virus.";
 RL J. Virol. 62:4627-4633 (1988).
 DR EMBL; M25399; AAA42548.1; -; Genomic_DNA.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1033 MW; 83AED7673411B5A1 CRC64;
 Query Match 32.7%; Score 16; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 STAPPV 6
 DB 3 STRLPV 8

RESULT 23
 ID P83492_BIOOC
 AC P83492; BIOOC PRELIMINARY; PRT; 7 AA.
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Alkaline protease Gr3 (EC 3.4.21.-) (Fragment).
 OS Bionectria ochroleuca (Gliocladium roseum).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.
 OX NCBI_TaxID=29856;
 RN [1]

RP PROTEIN SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.
 RC STRAIN=Gr87;
 RA Zhao M., Zhang K.;
 RL Submitted (DEC-2002) to Swiss-Prot.
 CC -!- FUNCTION: Acts as a serine protease.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
 DR InterPro; IPR000209; Pept S8_S53.
 DR PROSITE; PS00136; SUBTILASE_ASP; PARTIAL.
 DR PROSITE; PS00137; SUBTILASE_HIS; PARTIAL.
 DR PROSITE; PS00138; SUBTILASE_SER; PARTIAL.
 KW Hydrolase; Serine protease.
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 688 MW; 776DD455A6C1ADB0 CRC64;
 Query Match 30.6%; Score 15; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 STAP 4
 DB 4 SNAP 7

RESULT 24
 ID ACI_THUAL
 AC ACI_THUAL STANDARD; PRT; 8 AA.
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Angiotensin-converting enzyme inhibitor.
 OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OX NCBI_TaxID=8236;
 RN [1]

RP PROTEIN SEQUENCE.
 RC TISSUE=Muscle;
 RX MEDLINE=88326322; PubMed=3415688;
 RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;

RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
muscle."; Biophys. Res. Commun. 155:332-337(1988).
RL Biochem. J. 283 (Pt 3):813-821(1992).
CC -!- FUNCTION: Inhibits angiotensin-converting enzyme.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
CC PIR; A31570; A31570.
DR Direct protein sequencing; Metalloenzyme inhibitor;
KW Metalloprotease inhibitor. 6A863733051F1B7 CRC64;
SQ SEQUENCE 8 AA; 953 MW; 6A863733051F1B7 CRC64;
Query Match 30.6%; Score 15; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PVH 7
DB 1 PTH 3

RESULT 25

ID PPK2_PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-MAY-2005 (Rel. 47, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPR-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Blattellinae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=97353923; PubMed=9210163; DOI=10.1016/S0196-9781(97)00067-3;
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tissue-specific distribution of FXPRLamides in the nervous system of
the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
activity).
CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI; RANGE=1-8; NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
CC InterPro: IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Amidation; Direct protein sequencing; Neuropeptide; Pyrokinin.
FT MOD_RES 8 Leucine amide.
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 30.6%; Score 15; DB 1; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 APP 5
DB 1 SPP 3

RESULT 26

ID Q6JORS_PARLI PRELIMINARY; PRT; 8 AA.
AC Q6JORS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AUF1 similar protein (Fragment).
OS Paracentrotus lividus (Common sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
OC Paracentrotus.
OX NCBI_TaxID=7856;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15715964;
RA Pulcrano G., Leonardo R., Antiello F., Mancini P., Piscopo M.,
RA Branno M., Fucci L.;
RT "PLAUF is a novel P. lividus sea urchin RNA-binding protein.";
RL Gene 347:99-107(2005).
DR EMBL; AY609061; AAT37156.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 8 AA; 816 MW; 83C7633DC1A865A6 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAPP 5
DB 4 TAKP 7

RESULT 27

ID Q7M1V6_SOLTU PRELIMINARY; PRT; 8 AA.
AC Q7M1V6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lectin (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP PROTEIN SEQUENCE.
RA Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R.,
RA Bolwell G.P.;
RT "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber.
Characterization, immunolocalization and effects of wounding.";
RL Biochem. J. 283:813-821(1992).
RN [2]
RP PROTEIN SEQUENCE.
RX PubMed=1590771;
RA Millar D.J., Allen A.K., Smith C.G., Sidebottom C., Slabas A.R.,
RA Bolwell G.P.;
RT "Chitin-binding proteins in potato (Solanum tuberosum L.) tuber.
Characterization, immunolocalization and effects of wounding.";
RL Biochem. J. 283 (Pt 3):813-821(1992).
DR PIR; S21288; S21288.
FT NON_TER 1
SQ SEQUENCE 8 AA; 771 MW; C3775A71B5BDDA CRC64;

Query Match 30.6%; Score 15; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 APP 5
 :||
 6 SPP 8

Db

RESULT 28

Q9UCS8 HUMAN
 ID Q9UCS8_HUMAN PRELIMINARY; PRT; 9 AA.

AC Q9UCS8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Apolipoprotein A-I (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=92075698; PubMed=1742316; DOI=10.1016/0005-2760(91)90167-G;
 RA Enholm C., Bozas S.E., Tenkanen H., Kirzbaum L., Metso J.,
 RA Murphy B., Walker I.D.;
 RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40
 RT protein of human blood are different proteins which both bind to
 RT apolipoprotein A-I";
 RL Biochim. Biophys. Acta 1086:255-260(1991).
 DR GO; GO:0005576; C:extracellular region; ISS.
 DR GO; GO:0005319; F:lipid transporter activity; NAS.
 DR GO; GO:0008203; P:cholesterol metabolism; ISS.
 DR GO; GO:0006869; F:lipid transport; ISS.
 FT NON TER 1
 FT NON TER 9
 SQ SEQUENCE 9 AA; 981 MW; 7FE37775A6C7776B CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 APP 5
 :||
 6 SPP 8

Db

RESULT 29

Q16605 HUMAN
 ID Q16605_HUMAN PRELIMINARY; PRT; 9 AA.

AC Q16605;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE GST2 protein (Glutathione S-transferase) (Fragment).
 GN Name=GST2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=3138230;
 RA Chow N.W., Whang-Peng J., Kao-Shan C.S., Tam M.F., Lai H.-C.J.,
 RA Tu C.-P.D.;
 RT "Human glutathione S-transferases. The Ha multigene family encodes
 RT products of different but overlapping substrate specificities";
 RL J. Biol. Chem. 263:12797-12800(1988).
 DR EMBL; M21867; AAA52617.1; -; Genomic DNA.
 DR EMBL; M21866; AAA35938.1; -; Genomic DNA.

DR GO; GO:0004364; F:glutathione transferase activity; NAS.
 DR GO; GO:0009636; P:response to toxin; NAS.
 KW Transferase.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1116 MW; D168E72327633B1D CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.2e+06;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PPVH 7
 :||
 5 PKLH 8

Db

RESULT 30

Q7M3S5 TRYP
 ID Q7M3S5_TRYP PRELIMINARY; PRT; 9 AA.

AC Q7M3S5;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Phosphoenolpyruvate carboxykinase.
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95284106; PubMed=7766679; DOI=10.1016/0167-4838(95)00061-X;
 RA Hunt M., Koehler P.;
 RT "Purification and characterization of phosphoenolpyruvate
 RT carboxykinase from Trypanosoma brucei";
 RL Biochim. Biophys. Acta 1249:15-22(1995).
 DR PIR; S55696; S55696.
 SQ SEQUENCE 9 AA; 1063 MW; 35F2244331E05047 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.2e+06;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PPVH 7
 :||
 2 PIH 5

Db

RESULT 31

Q7R8X5 PLAYO
 ID Q7R8X5_PLAYO PRELIMINARY; PRT; 9 AA.

AC Q7R8X5;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=PY07095;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shalim S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoab A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite Plasmodium yoelii yoelii.";

RL Nature 419:512-519 (2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABJ01002528; EAA19452.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 9 AA; 1013 MW; 4684D44724441E7 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VHN 8
 Db 2 LHN 4

RESULT 32

ID Q4X981_PLACH PRELIMINARY; PRT; 9 AA.
 AC Q4X981;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC404684.00.0;
 OS Plasmodium chabaudi.
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Trueman H.E., Mendoza J.,
 RA Quail M.A., Ormond D., Doggett J., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Bidwell S.L., Rajandream M.A., Turner C.M.R., Waters A.P., Sinden R.S.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RA "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAJ01008648; CAH86543.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 1010 MW; 495F4441B6905727 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VHN 8
 Db 5 MHN 7

RESULT 33

ID Q4YFU0_PLABE PRELIMINARY; PRT; 9 AA.
 AC Q4YFU0;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE Hypothetical protein.
 GN ORFNames=PB404205.00.0;
 OS Plasmodium berghei.
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5821;
 RN NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAI01005534; CAI03128.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 9 AA; 1089 MW; AE5FD1E04B476056 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.2e+06;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PPVH 7
 Db 4 PYIH 7

RESULT 34

ID Q5G6L3_RHIHA PRELIMINARY; PRT; 9 AA.
 AC Q5G6L3;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE Amyloid beta protein (Fragment).
 GN Name=APP;
 OS Rhinopoma hardwickei (Lesser mouse-tailed bat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Laurasiatheria; Chiroptera; Microchiroptera;
 CC Rhinopomatidae; Rhinopoma.
 OX NCBI_TaxID=124756;
 RN NUCLEOTIDE SEQUENCE.
 RX PubMed=15681385; DOI=10.1126/science.1105113;
 RA Teeling E.C., Springer M.S., Madsen O., Bates P., O'Brien S.J.,
 RA Murphy W.J.;
 RT "A molecular phylogeny for bats illuminates biogeography and the
 RT fossil record."
 RL Science 307:580-584(2005).
 DR EMBL; AY834465; AAV92991.1; -; Genomic_DNA.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 1243 MW; 5D3CE868DB19C9C3 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VHN 8
 Db 7 MHN 9

RESULT 35

ID O81962_9FLOR PRELIMINARY; PRT; 9 AA.
 AC O81962;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit
 DE (Fragment).
 GN Name=rbcl;
 OS Caloglossa apomeiotica.
 CC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
 CC Caloglossa.
 OX NCBI_TaxID=76904;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=910;
 RA Kamiya M., West J.A., King R.J., Zuccarello G.C., Tanaka J., Hara Y.;
 RT "Evolutionary divergence in the red algae Caloglossa lepriurii and C.
 apomeiotica.";
 RL J. Phycol. 34:361-370(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=910;
 RA Kamiya M., Tanaka J., King R.J., West J.A., Zuccarello G.C., Kawai H.;
 RT "Reproductive and genetic distinction between broad and narrow
 entities of Caloglossa continua (Delesseriaceae, Rhodophyta).";
 RL Phycologia 38:356-367(1999).
 DR EMBL; D89948; BAA31281.1; -; Genomic_DNA.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;

Best Local Similarity 60.0%; Pred. No. 2.2e+06;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVHNV 9

Db 5 PTANV 9

RESULT 36

O81964_9FLOR PRELIMINARY; PRT; 9 AA.

AC O81964; Q9T388;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)

DE Ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit

DE (Fragment).;

GN Name=rbcl;

OS Caloglossa continua.

OG Chloroplast.

OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;

OC Caloglossa.

OX NCBI_TaxID=76905;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=639;

RA Kamiya M., West J.A., King R.J., Zuccarello G.C., Tanaka J., Hara Y.;

RT "Evolutionary divergence in the red algae Caloglossa lepriurii and C.

apomeiotica.";

RL J. Phycol. 34:361-370(1998).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=639, 500, and 729;

RA Kamiya M., Tanaka J., King R.J., West J.A., Zuccarello G.C., Kawai H.;

RT "Reproductive and genetic distinction between broad and narrow

entities of Caloglossa continua (Delesseriaceae, Rhodophyta).";

RL Phycologia 38:356-367(1999).

DR EMBL; D89950; BAA31285.1; -; Genomic_DNA.

DR EMBL; AB023379; BAA88908.1; -; Genomic_DNA.

DR EMBL; AB023380; BAA88910.1; -; Genomic_DNA.

DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

FT NON TER 1

SQ SEQUENCE 9 AA; 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;

Best Local Similarity 60.0%; Pred. No. 2.2e+06;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVHNV 9

Db 5 PTANV 9

RESULT 37

O81966_9FLOR

ID O81966_9FLOR PRELIMINARY; PRT; 9 AA.

AC O81966; Q9TJ87;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)

DE Ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit

DE (Fragment).;

GN Name=rbcl;

OS Caloglossa monosticha.

OG Chloroplast.

OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;

OC Caloglossa.

OX NCBI_TaxID=76906;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=892;

RA Kamiya M., West J.A., King R.J., Zuccarello G.C., Tanaka J., Hara Y.;

RT "Evolutionary divergence in the red algae Caloglossa lepriurii and C.

apomeiotica.";

RL J. Phycol. 34:361-370(1998).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=892, and 987;

RA Kamiya M., Tanaka J., King R.J., West J.A., Zuccarello G.C., Kawai H.;

RT "Reproductive and genetic distinction between broad and narrow

entities of Caloglossa continua (Delesseriaceae, Rhodophyta).";

RL Phycologia 38:356-367(1999).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=D571;

RA West J.A., Zuccarello G.C., Kamiya M.;

RT "Reproductive patterns of Caloglossa species (Delesseriaceae.

Rhodophyta) from Australia and New Zealand: multiple origins of

asexuality in C. lepriurii. Literature review on apomixis, mixed-

phase, bisexuality and sexual compatibility.";

RL Phycol. Res. 49:183-200(2001).

DR EMBL; D89960; BAA31305.1; -; Genomic_DNA.

DR EMBL; AF340178; AAK98083.1; -; Genomic_DNA.

DR EMBL; AF340179; AAK98085.1; -; Genomic_DNA.

DR EMBL; AF340180; AAK98087.1; -; Genomic_DNA.

DR EMBL; AB023381; BAA88912.1; -; Genomic_DNA.

DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

FT NON TER 1

SQ SEQUENCE 9 AA; 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;

Best Local Similarity 60.0%; Pred. No. 2.2e+06;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVHNV 9

Db 5 PTANV 9

RESULT 38

O81968_9FLOR

ID O81968_9FLOR PRELIMINARY; PRT; 9 AA.

AC O81968; Q95BY3;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)

DE Ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit

DE (Fragment).;

GN Name=rbcl;

OS Caloglossa ogasawaraensis.

OG Chloroplast.

OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;

OC Caloglossa.

OX NCBI_TaxID=76907;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=596;
 RA Kamiya M., West J.A., King R.J., Zuccarello G.C., Tanaka J., Hara Y.;
 RT "Evolutionary divergence in the red algae *Caloglossa lepreurii* and C.
 RT *aponeiotes*";
 RL J. Phycol. 34:361-370(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=596;
 RA Kamiya M., Tanaka J., King R.J., West J.A., Zuccarello G.C., Kawai H.;
 RT "Reproductive and genetic distinction between broad and narrow
 RT entities of *Caloglossa continua* (Delesseriaceae, Rhodophyta).";
 RL Phycologia 38:356-367(1999).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA West J.A., Zuccarello G.C., Kamiya M.;
 RT "Reproductive patterns of *Caloglossa* species (Delesseriaceae,
 RT Rhodophyta) from Australia and New Zealand: multiple origins of
 RT asexuality in C. lepreurii. Literature review on apomixis, mixed-
 RT phase, bisexuality and sexual compatibility.";
 RL Phycol. Res. 49:183-200(2001).
 DR EMBL: D89961; BAA31307.1; -: Genomic DNA.
 DR EMBL: AF340182; AAK98091.1; -: Genomic DNA.
 DR GO: GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 9 AA; 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVHNV 9
 |
 |
 |
 Db 5 PTANV 9

RESULT 39
 ID Q6EUV8 GERHY PRELIMINARY; PRT; 9 AA.
 AC Q6EUV8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Gerbera hybrida.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Asterales; Asteraceae; Mutisioideae; Mutisieae; Gerbera.
 OC NCBI_TaxID=18101;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Uimari A., Kotilainen M., Elomaa P., Yu D., Albert V.A., Teeri T.H.;
 RT "Integration of reproductive meristem fates by a SEPALLATA-like MADS
 RT box gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:15817-15822(2004).
 DR EMBL: AJ784156; CAH04877.1; -: mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 9 AA; 1108 MW; 151D41F5A401F1A0 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 HNV 9
 |
 |
 |
 Db 7 HNL 9

RESULT 40
 ID Q76FS7_9FLOR PRELIMINARY; PRT; 9 AA.
 AC Q76FS7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Rubisco large subunit (Fragment).
 GN Name=rbcl;
 OS Hypnea japonica.
 OG Chloroplast.
 OC Eukaryota; Rhodophyta; Florideophyceae; Gigartinales; Hypneaceae;
 OC Hypnea.
 OX NCBI_TaxID=105606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Yano T., Kamiya M., Arai S., Kawai H.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB104706; BAC82415.1; -: Genomic DNA.
 DR GO: GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 9 AA; 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVHNV 9
 |
 |
 |
 Db 5 PTANV 9

RESULT 41
 ID Q8HB43_9FLOR PRELIMINARY; PRT; 9 AA.
 AC Q8HB43;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Ribulose-1,5-bisphosphate large subunit (Fragment).
 GN Name=rbcl;
 OS Gracilaria perplexa.
 OC Chloroplast.
 OC Eukaryota; Rhodophyta; Florideophyceae; Gracilariaceae; Gracilariaceae;
 OC Gracilaria.
 OX NCBI_TaxID=197869;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Byrne K., Zuccarello G.C., West J.A., Liao M.-L., Kraft G.;
 RT "Gracilaria species (Gracilariaceae, Rhodophyta) from southeastern
 RT Australia, including a new species, *G. perplexa* sp. nov.: Morphology,
 RT molecular relationships and agar content.";
 RL Phycol. Res. 50:295-311(2002).
 DR EMBL: AY131306; AAN07038.1; -: Genomic DNA.
 DR EMBL: AY131307; AAN07040.1; -: Genomic DNA.
 DR EMBL: AY131308; AAN07042.1; -: Genomic DNA.
 DR GO: GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER
 SQ SEQUENCE 9 AA; 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.2e+06;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVHNV 9
 |
 |
 |
 Db 5 PTANV 9

RESULT 42
 ID Q8HB44_9FLOR PRELIMINARY; PRT; 9 AA.
 AC Q8HB44;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)


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DE Ribulose-1,5-bisphosphate large subunit (Fragment).
GN Name=rbcl;
OS Gracilaria cliftonii.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Gracilariales; Gracilariaceae;
OC Gracilaria.
OX NCBI_taxid=206548;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bryne K., Zuccarello G.C., West J.A., Liao M.-L., Kraft G.;
RT "Gracilaria species (Gracilariaceae, Rhodophyta) from southeastern
RT Australia, including a new species, G. perplexa sp. nov.: Morphology,
RT molecular relationships and agar content.";
RL Phycol. Res. 50:295-311(2002).
DR EMBL; AY131302; AAN07030.1; -; Genomic DNA.
DR EMBL; AY131303; AAN07032.1; -; Genomic DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 9 AA; 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVHNV 9
Db 5 PTANV 9

RESULT 43
Q8HB45 GRACH PRELIMINARY; PRT; 9 AA.
AC Q8HB45;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE Ribulose-1,5-bisphosphate large subunit (Ribulose-1,5-bisphosphate
DE carboxylase/oxygenase large subunit) (Fragment).
GN Name=rbcl;
OS Gracilaria chilensis (Red alga).
OG Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Gracilariales; Gracilariaceae;
OC Gracilaria.
OX NCBI_taxid=2775;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bryne K., Zuccarello G.C., West J.A., Liao M.-L., Kraft G.;
RT "Gracilaria species (Gracilariaceae, Rhodophyta) from southeastern
RT Australia, including a new species, G. perplexa sp. nov.: Morphology,
RT molecular relationships and agar content.";
RL Phycol. Res. 50:295-311(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Cohen S., Faugeron S., Martinez E.A., Correa J.A., Viard F.,
RA Destombe C., Valero M.;
RT "Molecular identification of two sibling species under the name
RT Gracilaria chilensis (Rhodophyta, Gracilariales).";
RL J. Phycol. 40:742-747(2004).
DR EMBL; AY131299; AAN07024.1; -; Genomic DNA.
DR EMBL; AY131300; AAN07026.1; -; Genomic DNA.
DR EMBL; AY131301; AAN07028.1; -; Genomic DNA.
DR EMBL; AY423840; AAR84581.1; -; Genomic DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 9 AA; 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVHNV 9
Db 5 PTANV 9

us-10-019-513-1.szlml9.rup
Db 5 PTANV 9

RESULT 44
Q8HRJ8 9FLOR PRELIMINARY; PRT; 9 AA.
AC Q8HRJ8;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Ribulose-1,5-bisphosphate large subunit (Fragment).
GN Name=rbcl;
OS Ptilophora prolifera.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Gelidiales; Gelidiaceae;
OC Ptilophora.
OX NCBI_taxid=143014;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bryne K., Zuccarello G.C., West J.A., Liao M.-L., Kraft G.;
RT "Gracilaria species (Gracilariaceae, Rhodophyta) from southeastern
RT Australia, including a new species, G. perplexa sp. nov.: Morphology,
RT molecular relationships and agar content.";
RL Phycol. Res. 50:295-311(2002).
DR EMBL; AY131312; AAN07050.1; -; Genomic DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 9 AA; 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVHNV 9
Db 5 PTANV 9

RESULT 45
Q8HRK0 9FLOR PRELIMINARY; PRT; 9 AA.
AC Q8HRK0;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Ribulose-1,5-bisphosphate large subunit (Fragment).
GN Name=rbcl;
OS Gracilaria secundata.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Gracilariales; Gracilariaceae;
OC Gracilaria.
OX NCBI_taxid=172973;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bryne K., Zuccarello G.C., West J.A., Liao M.-L., Kraft G.;
RT "Gracilaria species (Gracilariaceae, Rhodophyta) from southeastern
RT Australia, including a new species, G. perplexa sp. nov.: Morphology,
RT molecular relationships and agar content.";
RL Phycol. Res. 50:295-311(2002).
DR EMBL; AY131311; AAN07048.1; -; Genomic DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 9 AA; 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PVHNV 9
Db 5 PTANV 9

```

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Db          5 PTANV 9

RESULT 46
Q8HSL0_9FLOR PRELIMINARY;          PRT;          9 AA.
AC Q8HSL0_
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
  (Fragment).
GN Name=rbcl;
OS Murrayella pericladus.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Rhodomelaceae;
OC Murrayella.
OX NCBI_TaxID=110473;
RN [1]_TaxID=110473;
RP NUCLEOTIDE SEQUENCE.
RA Zuccarello G.C., Sandercock B., West J.A.;
  Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AF458764; AA014538.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVHNV 9
Db | | |
5 PTANV 9

RESULT 47
Q8HSL5_9FLOR PRELIMINARY;          PRT;          9 AA.
AC Q8HSL5_
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit
  (Fragment).
GN Name=rbcl;
OS Spvridia filamentosa.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Ceramiaceae;
OC Spvridia.
OX NCBI_TaxID=196632;
RN [1]_TaxID=196632;
RP NUCLEOTIDE SEQUENCE.
RA Zuccarello G.C., Sandercock B., West J.A.;
  Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AF458738; AA014515.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVHNV 9
Db | | |
5 PTANV 9

RESULT 48
Q8MDU2_9FLOR PRELIMINARY;          PRT;          9 AA.
AC Q8MDU2_
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
  (Fragment).
GN Name=rbcl;
OS Hypnea sp.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Gigartinales; Hypneaceae;
OC Hypnea.
OX NCBI_TaxID=196372;
RN [1]_TaxID=196372;
RP NUCLEOTIDE SEQUENCE.
RA Zuccarello G.C., West J.A., Ruess J.;
  "Phylogeography of the cosmopolitan red alga Caulacanthus ustulatus
  (Caulacanthaceae, Gigartinales).";
  Phycol. Res. 50:163-172(2002).
RL EMBL; AF453729; AM69942.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVHNV 9
Db | | |
5 PTANV 9

RESULT 49
Q8ME56_9RHOD PRELIMINARY;          PRT;          9 AA.
AC Q8ME56_
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
  (Fragment).
GN Name=rbcl;
OS Porphyra miniata.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Porphyra.
OX NCBI_TaxID=35147;
RN [1]_TaxID=35147;
RP NUCLEOTIDE SEQUENCE.
RA Teadale B.W., West A., Taylor H., Klein A.S.;
  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AF414600; AA03007.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 1 1 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 30.6%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PVHNV 9
Db | | |
5 PTANV 9

RESULT 50
Q8ME58_9RHOD PRELIMINARY;          PRT;          9 AA.
AC Q8ME58_
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
DE (Fragment).
GN Name=rbcL;
OS Porphyra linearis.
OC Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
OX NCBI_TaxID=60544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Teasdale B.W., West A., Taylor H., Klein A.S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF414598; AAN03005.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 9 AA; 977 MW; CA1A4DC1B771AB02 CRC64;
Query Match 30.6%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 PVHNV 9
Db 5 PTANV 9

Search completed: February 24, 2006, 10:18:15
Job time : 247 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 24, 2006, 10:14:46 ; Search time 38 Seconds
(without alignments)
22.788 Million cell updates/sec

Title: US-10-019-513-1

Perfect score: 49

Sequence: 1 STAPPVHV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	36.7	8	B39745	endoglycosylcerami
2	18	36.7	9	B41983	orf downreg to b
3	17	34.7	5	B37988	acid proteinase li
4	17	34.7	9	PC7078	unidentified 18.7K
5	16	32.7	7	E61491	seed protein 18-5
6	16	32.7	8	PT0530	T-cell receptor be
7	16	32.7	8	PT0559	T-cell receptor be
8	16	32.7	8	S43971	tumor-associated a
9	15	30.6	8	S21288	lectin - potato (1
10	15	30.6	8	A31570	angiotensin-conver
11	15	30.6	9	B30572	T-cell receptor be
12	15	30.6	9	S55696	phosphoenolpyruvat
13	14	28.6	7	P00727	H2 class I protein
14	14	28.6	7	S71299	ICL2 protein - Par
15	14	28.6	7	S9027	carboxylesterase (
16	14	28.6	7	PT0283	Ig heavy chain CRD
17	14	28.6	7	A61081	tryptophyllin, bas
18	14	28.6	8	S16324	hypothetical prote
19	14	28.6	8	S10783	enamelin f - bovin
20	14	28.6	8	E47393	neuropeptide calla
21	14	28.6	9	S65433	bradykinin - horn
22	14	28.6	9	B38740	Ig kappa chain C r
23	14	28.6	9	S26508	collagen alpha 2(V
24	14	28.6	9	A43065	hydroxyproline-3-b
25	14	28.6	9	PC7073	ubiquinol-cytochro
26	14	28.6	9	B60246	ornitho-kinin - ch
27	14	28.6	9	A26744	bradykinin-like pe
28	14	28.6	9	A61057	Thr-6 bradykinin -
29	14	28.6	9	A60579	bradykinin-like pe

bradykinin - commo
bradykinin-like pe
orf 2 rara 5'-regi
mosquitocidal toxi
T-cell receptor be
choline oxidase (E
vitrotoxin - destro
phenol 2-monooxyge
hypothetical prote
subesophageal gang
bHLH transcription
Ig heavy chain CRD
large granule L3 c
Ig heavy chain CRD
tetrameric protein
phosphoenolpyruvat
endosperm protein,
Ig heavy chain CRD
carbon-monoxide de
venom protein HR-3
N-methylpurine DNA
phagocytosis-stimu
RPCR-related neuro
ribosomal protein
peptidyl-dipectida
major protein anti
major protein anti
angiotensin-conver
ribulose-bisphosph
phosphoprotein, bo
flagellar protein
bradykinin-potenti
28K ubiquitin-immu
repetitive protein
contraction-inhibi
orf 3 rara 5'-regi
gene c-rel protein
glycoprotein compo
neural cell adhesi
neural cell adhesi
citrate synthase -
glycine reductase
unidentified 6.5/3
major postsynaptic
glutathione transf
isotocin - common
ribosomal protein
disseminatory sulf
photosystem II pro
cardioactive pepti
Ig heavy chain CRD
zymogen granule me
ATPase R1 subunit
transaldolase (EC
transaldolase (EC
calliWRamide 5 -
118K stomach cance
alpha-2-macroglobu
3-oxoacid CoA-tran
pev-tachykinin - p
orf 1 rara 5'-regi
copper resistance
alcohol dehydrogen
T-cell receptor be
halo-toxin - Pseud
angiotensin-conver
T-cell receptor be
T-cell receptor be
membrane protein -
hypothetical prote
omega-gliadine 1'
acetylcholinestera
aggreacan - bovine

103	10	20.4	7	2	PH0932	T-cell receptor be	176	9	18.4	9	2	PT0285	Ig heavy chain CRD
104	10	20.4	7	2	PH0029	pev-kinin 1 - pena	177	9	18.4	9	2	S78420	ribosomal protein
105	10	20.4	7	2	I46868	alpha-myosin heavy	178	9	18.4	9	2	PH0943	T-cell receptor be
106	10	20.4	7	2	ECMUCR	catch-relaxing pep	179	9	18.4	9	2	PH0937	T-cell receptor be
107	10	20.4	8	2	PT0368	Ig gamma chain C r	180	9	18.4	9	2	S39767	cardioactive pepi
108	10	20.4	8	2	I57532	gene Thislow prote	181	9	18.4	9	2	S56004	glucan 1,3-beta-gl
109	10	20.4	8	2	A61328	trypsin (EC 3.4.21	182	9	18.4	9	2	S39040	lysine-conopressin
110	10	20.4	8	2	S43972	tumor-associated a	183	9	18.4	9	2	A31576	xylose isomerase (
111	10	20.4	9	2	S13636	coat protein beta	184	9	18.4	9	2	A36363	cardioactive pepri
112	10	20.4	9	2	S36898	ribosomal protein	185	9	18.4	9	2	S27233	cardioactive pepri
113	10	20.4	9	2	A53797	3',5'-cyclic-GMP p	186	9	18.4	9	2	S06375	arginine vasotocin
114	10	20.4	9	2	PT0326	Ig heavy chain CRD	187	9	18.4	9	2	B61364	vasotocin - common
115	10	20.4	9	2	B46250	alpha-adaptin - bo	188	9	18.4	9	2	JQ0914	MHC class I histoc
116	10	20.4	9	2	PH0902	T-cell receptor be	189	9	18.4	9	2	I46016	cytokeratin 4 - bo
117	10	20.4	9	2	G58502	kidney and bladder	190	8	16.3	3	3	GRHU	growth-modulating
118	10	20.4	9	2	JF0073	ribosomal protein	191	8	16.3	3	3	RHPGT	thyroliberin - pig
119	10	20.4	9	2	PC2021	oxytocin-related p	192	8	16.3	3	3	A60898	thyroliberin - pig
120	10	20.4	9	2	I54379	gene NF2 protein -	193	8	16.3	3	3	RHSHT	thyroliberin - she
121	10	20.4	9	2	JQ1202	leader peptide - p	194	8	16.3	3	3	A92971	thyroliberin - eas
122	9	18.4	3	3	I50412	gene p20K protein	195	8	16.3	3	3	RHTD70	thyroliberin - Bom
123	9	18.4	4	2	PT0675	T-cell receptor be	196	8	16.3	4	2	A48360	gamma subunit of P
124	9	18.4	5	2	S51077	alpha-amylase - ri	197	8	16.3	4	2	I38888	COI intron 16 prot
125	9	18.4	5	2	PT0659	T-cell receptor be	198	8	16.3	4	2	PL0140	carbon-monoxide de
126	9	18.4	5	2	I40698	biotin B - Citroba	199	8	16.3	4	2	PT0712	T-cell receptor be
127	9	18.4	5	2	PT0686	T-cell receptor be	200	8	16.3	4	2	A32039	tyrosine-melanocyt
128	9	18.4	5	2	PT0669	T-cell receptor be	201	8	16.3	5	2	JN0860	peptidyl-dipeptida
129	9	18.4	5	4	A56728	serrawettin W2 - S	202	8	16.3	5	2	C41225	copper resistance
130	9	18.4	6	2	S14159	parasporal crystal	203	8	16.3	5	2	S70154	URF2 protein - Xan
131	9	18.4	6	2	S78764	ribosomal protein	204	8	16.3	5	2	JT0520	Ig kappa chain V-I
132	9	18.4	6	2	A19780	transferrin - bovi	205	8	16.3	5	2	A60521	glycogen phosphory
133	9	18.4	6	2	I49808	DP-2.5 region - m	206	8	16.3	6	2	JN0861	peptidyl-dipeptida
134	9	18.4	6	2	A64674	FC epsilon RIIB -	207	8	16.3	6	2	A61419	sarcosine dehydrog
135	9	18.4	6	2	PT0531	T-cell receptor be	208	8	16.3	6	2	B56979	collagen alpha 1(I
136	9	18.4	6	2	PT0643	T-cell receptor be	209	8	16.3	6	2	PT0693	T-cell receptor be
137	9	18.4	6	2	I49421	laminin B1 - weate	210	8	16.3	6	2	PT0709	T-cell receptor be
138	9	18.4	7	1	NVPG7	hypothalamic hepta	211	8	16.3	6	2	S71349	beta-crystallin B2
139	9	18.4	7	2	PT0515	T-cell receptor be	212	8	16.3	6	2	A27696	contraction-inhibi
140	9	18.4	7	2	PT0520	T-cell receptor be	213	8	16.3	6	4	A35039	hypothetical colla
141	9	18.4	7	2	PT0623	T-cell receptor be	214	8	16.3	7	2	JN0859	peptidyl-dipeptida
142	9	18.4	7	4	I56695	hypothetical L2 pr	215	8	16.3	7	2	S42407	gramicidin S synth
143	9	18.4	8	1	LFSAME	probable msrA lead	216	8	16.3	7	2	A28709	phosphonoacetaldeh
144	9	18.4	8	2	A33995	adipokinetic hormo	217	8	16.3	7	2	PT0087	ribulose-bisphosph
145	9	18.4	8	2	B44960	neuropeptide Led-C	218	8	16.3	7	2	I48105	dihydrofolate redu
146	9	18.4	8	2	S11545	adipokinetic hormo	219	8	16.3	7	2	I48086	DNA topoisomerase
147	9	18.4	8	2	S08996	hypertrehalosemic	220	8	16.3	7	2	E33932	Ig mu chain D regi
148	9	18.4	8	2	B49823	adipokinetic hormo	221	8	16.3	7	2	S66442	glutathione S-tran
149	9	18.4	8	2	A28004	adipokinetic hormo	222	8	16.3	7	2	A38081	amine oxidase (cop
150	9	18.4	8	2	T14906	hypothetical prote	223	8	16.3	7	2	A58718	carnocin UI49 - Ca
151	9	18.4	8	2	PT0639	T-cell receptor be	224	8	16.3	7	2	S29735	polyphosphate-gluc
152	9	18.4	8	2	B48823	olfactory receptor	225	8	16.3	7	2	A28340	myomodulin - Calif
153	9	18.4	8	2	A61597	cytochrome P450 AL	226	8	16.3	7	2	S08606	hypothetical prote
154	9	18.4	8	2	S65647	2-hydroxyglutaryl-	227	8	16.3	8	2	A44960	neuropeptide Led-C
155	9	18.4	8	2	S21273	cellulase (EC 3.2.	228	8	16.3	8	2	A61348	red pigment-concen
156	9	18.4	8	2	A46306	spasmogenic toxin	229	8	16.3	8	2	S08995	hypertrehalosemic
157	9	18.4	8	2	J50316	leucokinin VI - Ma	230	8	16.3	8	2	A49823	adipokinetic hormo
158	9	18.4	8	2	A32967	leucopyrokinin - M	231	8	16.3	8	2	S15422	adipokinetic hormo
159	9	18.4	8	2	S66646	cardioacceleratory	232	8	16.3	8	2	A43976	hypertrehalosemic
160	9	18.4	8	2	I49404	prealbumin - weate	233	8	16.3	8	2	B43976	hypertrehalosemic
161	9	18.4	8	2	A59028	MHC class I histoc	234	8	16.3	8	2	A58641	adipokinetic hormo
162	9	18.4	8	2	XGHUEU	urine glycopeptide	235	8	16.3	8	2	S68802	nitrate reductase
163	9	18.4	9	2	A93408	oxytocin - Austral	236	8	16.3	8	2	G33098	205K exoantigen -
164	9	18.4	9	2	A92774	oxytocin - spotted	237	8	16.3	8	2	PT0311	Ig heavy chain CRD
165	9	18.4	9	2	A93147	oxytocin - finback	238	8	16.3	8	2	B45800	serum albumin - do
166	9	18.4	9	2	A91466	oxytocin - hippopo	239	8	16.3	8	2	PH1618	Ig H chain V-D-J r
167	9	18.4	9	2	B90667	oxytocin - rabbit	240	8	16.3	8	2	PT0691	T-cell receptor be
168	9	18.4	9	2	A28495	conopressin G - co	241	8	16.3	8	2	A05169	neuropeptide M-I -
169	9	18.4	9	2	B28495	conopressin S - co	242	8	16.3	8	2	S21663	neuropeptide - flo
170	9	18.4	9	2	A61102	parathyroid hormon	243	8	16.3	8	2	I48934	apolipoprotein A-I
171	9	18.4	9	2	A60108	exotoxin A - Strep	244	8	16.3	8	2	A54823	olfactory receptor
172	9	18.4	9	2	A61230	calsequestrin, car	245	8	16.3	8	2	I57018	gene ctf protein
173	9	18.4	9	2	B33098	231K exoantigen -	246	8	16.3	8	2	S65381	cytochrome-c oxida
174	9	18.4	9	2	PT0231	Ig heavy chain CDR	247	8	16.3	8	2	A35180	neutral proteinase
175	9	18.4	9	2	PT0238	Ig heavy chain CRD	248	8	16.3	8	2	S69165	ferredoxin a2 - Ja

249	8	16.3	8	2	A25836	L-serine ammonia-1	322	7	14.3	8	2	A58620	adipokinetic hormo
250	8	16.3	8	4	I54017	granulocyte-colony	323	7	14.3	8	2	S55310	adipokinetic hormo
251	8	16.3	8	2	S07205	litorin 2-Glu - Au	324	7	14.3	8	2	S10596	adipokinetic hormo
252	8	16.3	9	2	S07204	litorin I - Austr	325	7	14.3	8	2	PH1407	Ig heavy chain V r
253	8	16.3	9	2	S07241	litorin - Rohde's	326	7	14.3	8	2	PL0184	capaid protein VP
254	8	16.3	9	2	E28854	fibrinopeptide B -	327	7	14.3	8	2	P70727	ipgr protein - Shi
255	8	16.3	9	2	JS0302	xenopsin-related p	328	7	14.3	8	2	S22428	chitin-binding pro
256	8	16.3	9	2	A03020	xenopsin-related p	329	7	14.3	8	2	A39892	P element, P cyt
257	8	16.3	9	2	S66608	quinoline 2-oxid	330	7	14.3	8	2	P70627	T-cell receptor be
258	8	16.3	9	2	T31612	hypothetical prote	331	7	14.3	8	2	P70509	T-cell receptor be
259	8	16.3	9	2	P70272	Ig heavy chain CRD	332	7	14.3	8	2	P70547	T-cell receptor be
260	8	16.3	9	2	S65913	pyrimidine synthe	333	7	14.3	8	2	P70716	T-cell receptor be
261	8	16.3	9	2	PH1591	Ig H chain V-D-J r	334	7	14.3	8	2	S29272	tocopherol-binding
262	8	16.3	9	2	A42266	peptidylglycine mo	335	7	14.3	8	2	S19288	acylase - Kluvyera
263	8	16.3	9	2	D57444	neuropeptide Grb-A	336	7	14.3	8	2	P70030	inulinase (EC 3.2.
264	8	16.3	9	2	A29477	diuretic neuropept	337	7	14.3	8	2	C61512	variant surface gl
265	8	16.3	9	2	C41978	calliFMRamide 3 -	338	7	14.3	8	2	JS0317	leucokinin VII - M
266	8	16.3	9	2	P70080	60K Ca binding pro	339	7	14.3	8	2	D47393	neuropeptide calla
267	8	16.3	9	2	I49406	bone gla protein -	340	7	14.3	8	2	S71919	alcohol dehydrogen
268	8	16.3	9	2	S99437	D-amino-acid oxida	341	7	14.3	8	2	A41117	acetylcholinestera
269	8	16.3	9	2	UN0026	sperm-activating p	342	7	14.3	8	2	A14683	aspartate transami
270	8	16.3	9	2	B45020	probable minipolyp	343	7	14.3	8	2	A28719	thymic humoral fac
271	8	16.3	9	4	I57650	hemoglobin alpha c	344	7	14.3	8	2	I48935	apolipoprotein A-I
272	7	14.3	3	3	A43391	TRH-like tripeptid	345	7	14.3	8	2	I64832	Ca2+-transporting
273	7	14.3	3	3	I78890	tyrosine protein k	346	7	14.3	8	2	B47449	neuropeptide B - b
274	7	14.3	3	3	A33802	thyrotropin-releas	347	7	14.3	9	2	B45796	dihydrolipoamide S
275	7	14.3	4	2	S53508	starvation-induced	348	7	14.3	9	2	D58503	translation elonga
276	7	14.3	4	2	I51049	metallothionein-A	349	7	14.3	9	2	S66607	quinoline 2-oxid
277	7	14.3	4	2	P70240	Ig heavy chain CRD	350	7	14.3	9	2	S01123	photosystem II 3.2
278	7	14.3	4	2	I54357	schwannomin - mous	351	7	14.3	9	2	S70345	amine oxidase (cop
279	7	14.3	4	2	A35779	neuropeptide Antho	352	7	14.3	9	2	P70288	Ig heavy chain CRD
280	7	14.3	5	1	H0ROHA	proctolin - Americ	353	7	14.3	9	2	P70324	Ig heavy chain CRD
281	7	14.3	5	2	B22565	R-phycoerythrin al	354	7	14.3	9	2	B49712	ATP-binding protei
282	7	14.3	5	2	A37114	hypoxanthine phosph	355	7	14.3	9	2	C60070	gastrin - domestic
283	7	14.3	5	2	S53595	hypothetical prote	356	7	14.3	9	2	G56978	collagen alpha 1(I
284	7	14.3	5	2	P70267	Ig heavy chain CRD	357	7	14.3	9	2	I58350	gene c-mpl protein
285	7	14.3	5	2	P70596	T-cell receptor be	358	7	14.3	9	2	S02384	probable membrane
286	7	14.3	5	2	H44817	34.5K structural p	359	7	14.3	9	2	A61620	locustamyotropin I
287	7	14.3	5	2	F44817	34.5K structural p	360	7	14.3	9	2	A41978	calliFMRamide 1 -
288	7	14.3	5	2	B44817	34.5K structural p	361	7	14.3	9	2	A44787	calliFMRamide 10
289	7	14.3	5	2	D44817	35K structural pro	362	7	14.3	9	2	B41978	calliFMRamide 2 -
290	7	14.3	5	2	A60411	proctolin - Atlant	363	7	14.3	9	2	D41978	calliFMRamide 4 -
291	7	14.3	6	2	A35890	RNA-directed DNA p	364	7	14.3	9	2	B20569	serum amyloid P-co
292	7	14.3	6	2	S11556	hydrogensulfite re	365	7	14.3	9	2	S77984	cytochrome-c oxida
293	7	14.3	6	2	A37765	hypothetical prote	366	7	14.3	9	2	B39504	octamer-binding pr
294	7	14.3	6	2	A61140	sperm acrosomal pr	367	7	14.3	9	2	S66635	alpha-2-macroglobu
295	7	14.3	6	2	I67345	MHC H2-K-k cell su	368	7	14.3	9	2	S10784	enamelin 1 - bovin
296	7	14.3	6	2	I65546	MHC H2-L antigen -	369	7	14.3	9	2	I46023	growth hormone rec
297	7	14.3	6	2	P70518	T-cell receptor be	370	7	14.3	9	2	S78762	ribosomal protein
298	7	14.3	6	2	P70616	T-cell receptor be	371	7	14.3	9	2	A28924	fructose-bisphosph
299	7	14.3	6	2	P70650	T-cell receptor be	372	7	14.3	9	2	PC7074	translation elonga
300	7	14.3	6	2	P70550	T-cell receptor be	373	7	14.3	9	2	S19329	sperm-activating p
301	7	14.3	6	2	I49424	cytotoxic T-lympho	374	7	14.3	9	2	S15850	vitamin D3 26-mono
302	7	14.3	7	1	A61324	dermorphin - Rohde	375	7	14.3	9	2	A60522	sperm-activating p
303	7	14.3	7	2	S36662	dermorphin (Lys-7)	376	6	12.2	3	3	P70636	T-cell receptor be
304	7	14.3	7	2	S21230	dermorphin (Trp-4,	377	6	12.2	4	2	A41890	protein D - Becher
305	7	14.3	7	2	PH1408	Ig heavy chain V r	378	6	12.2	4	2	S43014	hypothetical prote
306	7	14.3	7	2	A44428	platelet aggregati	379	6	12.2	4	2	A40135	branched-chain-ami
307	7	14.3	7	2	S78024	ribosomal protein	380	6	12.2	4	2	I40697	biotin A - Citroba
308	7	14.3	7	2	A33098	244K exoantigen -	381	6	12.2	5	2	B18136	20K protein - Rick
309	7	14.3	7	2	C56793	platelet glycoprot	382	6	12.2	5	2	JH0253	gut pentapeptide -
310	7	14.3	7	2	B39040	calsequestrin, fas	383	6	12.2	5	2	P70281	Ig heavy chain CRD
311	7	14.3	7	2	P70524	T-cell receptor be	384	6	12.2	5	2	PT0295	seminal plasma pro
312	7	14.3	7	2	P70526	T-cell receptor be	385	6	12.2	5	2	S62883	T-cell receptor be
313	7	14.3	7	2	P70521	T-cell receptor be	386	6	12.2	5	2	PT0651	T-cell receptor be
314	7	14.3	7	2	PT0683	glucuronosyltransf	387	6	12.2	5	2	PT0695	27.5 kda structura
315	7	14.3	7	2	FX0008	serine/threonine-s	388	6	12.2	5	2	G44817	27.5K structural p
316	7	14.3	7	2	S58797	major fat-globule	389	6	12.2	5	2	I44817	27.5K structural p
317	7	14.3	7	2	B48394	Na+-transporting A	390	6	12.2	5	2	E44817	28.5K structural p
318	7	14.3	7	2	S45648	pullulanase (EC 3.	391	6	12.2	5	2	C44817	28K structural pro
319	7	14.3	7	2	PN0649	calliFMRamide 11	392	6	12.2	5	2	A44817	tram protein - Esc
320	7	14.3	7	2	B44787	orf 4 rara 5'-regi	393	6	12.2	5	2	A32014	fulicin - giant Af
321	7	14.3	7	4	S15597		394	6	12.2	5	2	A44692	

395	6	12.2	5	2	PT0585	T-cell receptor be	468	5	10.2	5	2	139966	ribosomal protein
396	6	12.2	6	2	JT0355	lipopeptide WS1279	469	5	10.2	5	2	139965	ribosomal protein
397	6	12.2	6	2	S29637	jacalin beta-II ch	470	5	10.2	5	2	S70615	endo-1,4-beta-xyla
398	6	12.2	6	2	B61512	variant surface gl	471	5	10.2	5	2	S70615	R-phycoerythrin ga
399	6	12.2	6	2	A31263	dihydrofolate redu	472	5	10.2	5	2	T14908	hypothetical prote
400	6	12.2	6	2	B31263	cytochrome-c oxida	473	5	10.2	5	2	IS0385	myosin light chain
401	6	12.2	6	2	PT05332	T-cell receptor be	474	5	10.2	5	2	PT0308	ig heavy chain CRD
402	6	12.2	6	2	PT0587	T-cell receptor be	475	5	10.2	5	2	C53284	T-cell receptor be
403	6	12.2	6	2	PT0593	T-cell receptor be	476	5	10.2	5	2	PT0610	T-cell receptor be
404	6	12.2	6	2	S60293	tubulin beta-3 cha	477	5	10.2	5	2	PT0525	T-cell receptor be
405	6	12.2	6	2	PC4127	hypothetical 6 pro	478	5	10.2	5	2	PT0597	T-cell receptor be
406	6	12.2	6	2	PT0605	T-cell receptor be	479	5	10.2	5	2	PT0729	T-cell receptor be
407	6	12.2	6	2	A43129	neuropeptide GNFR	480	5	10.2	5	2	PT0624	T-cell receptor be
408	6	12.2	7	1	XEYDGD	galactose oxidase	481	5	10.2	5	2	PT0625	T-cell receptor be
409	6	12.2	7	2	S71867	glutathione transp	482	5	10.2	5	2	PT0672	T-cell receptor be
410	6	12.2	7	2	S16364	opacity protein P.	483	5	10.2	5	2	PT0660	T-cell receptor be
411	6	12.2	7	2	S16365	opacity protein P.	484	5	10.2	5	2	PT0656	T-cell receptor be
412	6	12.2	7	2	B34818	vicilin 57K chain	485	5	10.2	5	2	PT0535	T-cell receptor be
413	6	12.2	7	2	H33098	180K exoantigen -	486	5	10.2	5	2	PT0699	T-cell receptor be
414	6	12.2	7	2	PC2370	probable H+-transp	487	5	10.2	5	2	PT0553	T-cell receptor be
415	6	12.2	7	2	S45311	microcin C7 - Esch	488	5	10.2	5	2	PT0561	T-cell receptor be
416	6	12.2	7	2	S59622	glucose isomerase	489	5	10.2	5	2	PT0690	T-cell receptor be
417	6	12.2	8	2	S59622	metallothionein is	490	5	10.2	5	2	PT0684	T-cell receptor be
418	6	12.2	8	2	PA0035	protein QA300039 -	491	5	10.2	5	2	PT0590	T-cell receptor be
419	6	12.2	8	2	S78036	ribosomal protein	492	5	10.2	5	2	PT0577	T-cell receptor be
420	6	12.2	8	2	S13661	polygalacturonase	493	5	10.2	5	2	PT0580	T-cell receptor be
421	6	12.2	8	2	A42057	fibroblast growth	494	5	10.2	5	2	PT0700	T-cell receptor be
422	6	12.2	8	2	PT0588	T-cell receptor be	495	5	10.2	5	2	PT0713	T-cell receptor be
423	6	12.2	8	2	PH0934	T-cell receptor be	496	5	10.2	5	2	S69237	surface protein te
424	6	12.2	8	2	A37521	R-phycoerythrin ga	497	5	10.2	5	2	PT0644	T-cell receptor be
425	6	12.2	8	2	B27867	homeotic protein U	498	5	10.2	5	2	PT0600	T-cell receptor be
426	6	12.2	8	2	H41978	calliFERamide B -	499	5	10.2	5	2	PT0601	T-cell receptor be
427	6	12.2	8	2	A61467	penalumin - Adeli	500	5	10.2	5	2	PT0585	T-cell receptor be
428	6	12.2	8	2	T48890	hypothetical prote	501	5	10.2	5	2	PT0701	T-cell receptor be
429	6	12.2	8	2	E60588	sperm-activating p	502	5	10.2	5	2	PT0717	T-cell receptor be
430	6	12.2	9	1	YFPG	thymic factor - pi	503	5	10.2	5	3	JT0870	phytoaulfokine alp
431	6	12.2	9	1	AKLIQM	locustamyoinhibiti	504	5	10.2	6	2	S66195	alcohol dehydrogen
432	6	12.2	9	2	A60957	thymocyte growth p	505	5	10.2	6	2	S02617	alcohol dehydrogen
433	6	12.2	9	2	A24244	adipokinetic hormo	506	5	10.2	6	2	B34835	dnaa protein - Pse
434	6	12.2	9	2	D24180	fibronogen beta ch	507	5	10.2	6	2	JH0784	neuropeptide TE-6
435	6	12.2	9	2	C24180	fibronogen beta ch	508	5	10.2	6	2	B26206	alpha-1,4-glucan-p
436	6	12.2	9	2	F28854	fibriropeptide B -	509	5	10.2	6	2	I59142	platelet-derived g
437	6	12.2	9	2	D28854	fibriropeptide B -	510	5	10.2	6	2	PT0510	T-cell receptor be
438	6	12.2	9	2	S70334	endosporm protein.	511	5	10.2	6	2	PT0519	T-cell receptor be
439	6	12.2	9	2	PT0270	ig heavy chain CRD	512	5	10.2	6	2	PT0512	T-cell receptor be
440	6	12.2	9	2	PT0299	ig heavy chain CRD	513	5	10.2	6	2	PT0539	T-cell receptor be
441	6	12.2	9	2	PT0670	T-cell receptor be	514	5	10.2	6	2	PT0630	T-cell receptor be
442	6	12.2	9	2	PT0562	T-cell receptor be	515	5	10.2	6	2	PT0637	T-cell receptor be
443	6	12.2	9	2	I52974	seminal vesicle pr	516	5	10.2	6	2	PT0621	T-cell receptor be
444	6	12.2	9	2	PH0917	T-cell receptor be	517	5	10.2	6	2	PT0619	T-cell receptor be
445	6	12.2	9	2	PH0921	T-cell receptor be	518	5	10.2	6	2	PT0641	T-cell receptor be
446	6	12.2	9	2	S78426	52.5K protein - sp	519	5	10.2	6	2	PT0657	T-cell receptor be
447	6	12.2	9	2	S19523	orf AB protein - S	520	5	10.2	6	2	PT0662	T-cell receptor be
448	6	12.2	9	2	A57444	neuropeptide Grb-A	521	5	10.2	6	2	PT0668	T-cell receptor be
449	6	12.2	9	2	B57444	neuropeptide Grb-A	522	5	10.2	6	2	PT0648	T-cell receptor be
450	6	12.2	9	2	A45199	L-hyosophorin - Ja	523	5	10.2	6	2	PT0533	T-cell receptor be
451	6	12.2	9	2	PC7076	spectrin alpha cha	524	5	10.2	6	2	PT0720	T-cell receptor be
452	6	12.2	9	2	G85802	hypothetical prote	525	5	10.2	6	2	PT0560	T-cell receptor be
453	6	12.2	9	4	I73804	hypothetical E2 pr	526	5	10.2	6	2	PT0723	T-cell receptor be
454	5	10.2	3	3	PT0622	T-cell receptor be	527	5	10.2	6	2	PT0718	T-cell receptor be
455	5	10.2	3	3	T13892	cytochrome-c oxida	528	5	10.2	6	2	PT0589	T-cell receptor be
456	5	10.2	4	2	B43848	cell surface adhes	529	5	10.2	6	2	PT0730	T-cell receptor be
457	5	10.2	4	2	T30569	hypothetical prote	530	5	10.2	6	2	PD0028	pev-kinin 2 - pena
458	5	10.2	4	2	I57745	D-mannanase hydrol	531	5	10.2	6	2	S29881	Na+/K+-exchanging
459	5	10.2	4	2	PT0696	T-cell receptor be	532	5	10.2	6	2	A61068	locustakinin - mig
460	5	10.2	4	2	PT0645	T-cell receptor be	533	5	10.2	7	2	S19630	ribosomal protein
461	5	10.2	4	2	PT0661	T-cell receptor be	534	5	10.2	7	2	S20446	elastase - Pseudom
462	5	10.2	4	2	PT0534	T-cell receptor be	535	5	10.2	7	2	S25266	piig protein - Bac
463	5	10.2	4	2	PT0698	T-cell receptor be	536	5	10.2	7	2	PT0289	ig heavy chain CRD
464	5	10.2	4	2	PT0551	T-cell receptor be	537	5	10.2	7	2	E30608	ig kappa chain V-I
465	5	10.2	4	2	PT0697	T-cell receptor be	538	5	10.2	7	2	B33541	hypothetical prote
466	5	10.2	4	2	PT0566	T-cell receptor be	539	5	10.2	7	2	PH1602	ig H chain V-D-J r
467	5	10.2	5	2	I39964	ribosomal protein	540	5	10.2	7	2	PT0611	T-cell receptor be

541	5	10.2	7	2	PT0523	T-cell receptor be	614	4	8.2	4	2	I37013	protamine p1 - Cer
542	5	10.2	7	2	PT0628	T-cell receptor be	615	4	8.2	4	2	I84439	protamine p1 - sav
543	5	10.2	7	2	PT0642	T-cell receptor be	616	4	8.2	4	2	PL0146	carbon-monoxide de
544	5	10.2	7	2	PT0620	T-cell receptor be	617	4	8.2	4	2	JQ1273	neuropeptide Antho
545	5	10.2	7	2	PT0667	T-cell receptor be	618	4	8.2	4	2	A32480	achatin-I - giant
546	5	10.2	7	2	PT0663	T-cell receptor be	619	4	8.2	4	2	PT0271	Ig heavy chain CRD
547	5	10.2	7	2	PT0704	T-cell receptor be	620	4	8.2	4	2	PT0633	T-cell receptor be
548	5	10.2	7	2	PT0689	T-cell receptor be	621	4	8.2	4	2	PT0711	T-cell receptor be
549	5	10.2	7	2	PT0719	T-cell receptor be	622	4	8.2	4	2	PT0677	T-cell receptor be
550	5	10.2	7	2	PT0586	T-cell receptor be	623	4	8.2	4	2	PT0706	T-cell receptor be
551	5	10.2	7	2	PT0569	T-cell receptor be	624	4	8.2	4	2	PT0721	T-cell receptor be
552	5	10.2	7	2	PT0576	T-cell receptor be	625	4	8.2	4	2	B41225	copper resistance
553	5	10.2	7	2	PT0579	T-cell receptor be	626	4	8.2	5	2	I40702	primase - Citrobac
554	5	10.2	7	2	PT0581	T-cell receptor be	627	4	8.2	5	2	D37325	pap fibrial regul
555	5	10.2	7	2	PT0702	T-cell receptor be	628	4	8.2	5	2	D60274	major protein anti
556	5	10.2	7	2	PQ0777	NADH2 dehydrogenas	629	4	8.2	5	2	T14910	hypothetical prote
557	5	10.2	7	2	S09066	globulin IV alpha	630	4	8.2	5	2	S55237	zinc-binding prote
558	5	10.2	7	2	B35890	RNA-directed DNA p	631	4	8.2	5	2	A60803	neuropeptide - sea
559	5	10.2	7	2	PC1812	sex pheromone cCF1	632	4	8.2	5	2	B61168	cocoonase (EC 3.4
560	5	10.2	7	2	PC2132	FMRFamide-related	633	4	8.2	5	2	PT0278	Ig heavy chain CRD
561	5	10.2	7	2	S33244	neuromodulatory pe	634	4	8.2	5	2	B44823	synaptosomal-assoc
562	5	10.2	7	2	S33245	neuromodulatory pe	635	4	8.2	5	2	D44823	synaptosomal-assoc
563	5	10.2	7	2	S33246	neuromodulatory pe	636	4	8.2	5	2	PT0513	T-cell receptor be
564	5	10.2	7	2	PT0529	T-cell receptor be	637	4	8.2	5	2	PT0703	T-cell receptor be
565	5	10.2	7	2	PT0544	T-cell receptor be	638	4	8.2	5	2	PT0707	T-cell receptor be
566	5	10.2	7	4	I55382	hypothetical pepti	639	4	8.2	5	2	PT0573	T-cell receptor be
567	5	10.2	8	2	A32523	peptidyl-dipeptida	640	4	8.2	5	2	PT0572	T-cell receptor be
568	5	10.2	8	2	S63493	disseminatory sulf	641	4	8.2	5	2	PT0679	T-cell receptor be
569	5	10.2	8	2	PA0032	protein QA30040 -	642	4	8.2	5	2	S68326	blood cell protein
570	5	10.2	8	2	TU952	hypothetical prote	643	4	8.2	5	2	I40469	dnax2-like protein
571	5	10.2	8	2	PT0279	Ig heavy chain CRD	644	4	8.2	5	2	PT0608	T-cell receptor be
572	5	10.2	8	2	PH0803	T-cell receptor al	645	4	8.2	5	2	PT0538	T-cell receptor be
573	5	10.2	8	2	PT0595	T-cell receptor be	646	4	8.2	5	2	PT0540	T-cell receptor be
574	5	10.2	8	2	PT0522	T-cell receptor be	647	4	8.2	5	2	C32751	spinal cord peptid
575	5	10.2	8	2	PT0631	T-cell receptor be	648	4	8.2	5	2	A28830	mitosis inhibiting
576	5	10.2	8	2	PT0613	T-cell receptor be	649	4	8.2	6	2	A60986	N-formyl oligopept
577	5	10.2	8	2	A38887	T-cell receptor ga	650	4	8.2	6	2	T11779	phosphoglycerate t
578	5	10.2	8	2	B47594	aspartate kinase (651	4	8.2	6	2	S11024	R-phycocerythrin be
579	5	10.2	8	2	A61496	ubiquitin - celery	652	4	8.2	6	2	C22565	hydrogensulfate re
580	5	10.2	8	2	PC1002	leucine-tRNA ligas	653	4	8.2	6	2	A60494	antineoplastic gly
581	5	10.2	8	2	S37141	rpsA protein - Erw	654	4	8.2	6	2	I51434	H4 histone - Affic
582	5	10.2	8	2	D61512	variant surface gl	655	4	8.2	6	2	I37027	protamine p1 - gor
583	5	10.2	8	2	PL0162	paramyosin - north	656	4	8.2	6	2	I37263	pyruvate kinase (E
584	5	10.2	8	2	JS0315	leucokinin V - Mad	657	4	8.2	6	2	A11490	glycoprotein compo
585	5	10.2	8	2	A47618	beta-galactosidase	658	4	8.2	6	2	H48394	whely glycoprotein
586	5	10.2	8	2	S68325	blood cell protein	659	4	8.2	6	2	PC4392	fatty-acid synthas
587	5	10.2	8	2	S20162	leghemoglobin III	660	4	8.2	6	2	A20186	alpha-tubulin - Ch
588	5	10.2	9	2	A61357	phylocaerulein -	661	4	8.2	6	2	I48126	T-cell receptor be
589	5	10.2	9	2	A44873	caldesmon - rabbit	662	4	8.2	6	2	PT0629	T-cell receptor be
590	5	10.2	9	2	G41946	T-cell receptor ga	663	4	8.2	6	2	PT0514	T-cell receptor be
591	5	10.2	9	2	PH0935	T-cell receptor be	664	4	8.2	6	2	PT0516	T-cell receptor be
592	5	10.2	9	2	PH0918	T-cell receptor be	665	4	8.2	6	2	PT0604	T-cell receptor be
593	5	10.2	9	2	A43848	cell surface adhes	666	4	8.2	6	2	PT0687	T-cell receptor be
594	5	10.2	9	2	B39841	dextranucrase (EC	667	4	8.2	6	2	PT0652	T-cell receptor be
595	5	10.2	9	2	A39841	sucrose 3-glucosyl	668	4	8.2	6	2	PT0568	T-cell receptor be
596	5	10.2	9	2	S13333	alpha/beta-gliadin	669	4	8.2	6	2	PT0726	T-cell receptor be
597	5	10.2	9	2	UN0027	[Phe-6]-mosact - a	670	4	8.2	6	2	PT0727	T-cell receptor be
598	5	10.2	9	2	A61386	macrophage inhibit	671	4	8.2	6	2	F41946	T-cell receptor ga
599	5	10.2	9	2	S30494	cat gene leader pe	672	4	8.2	6	2	A41946	T-cell receptor ga
600	5	10.2	9	2	B24362	chloramphenicol O-	673	4	8.2	6	2	A49792	acylaminoacyl-pept
601	4	8.2	3	3	PQ0010	angiotensin-conver	674	4	8.2	6	2	PT0511	T-cell receptor be
602	4	8.2	3	3	PT0578	T-cell receptor be	675	4	8.2	6	2	A61411	acetylcholin - rat
603	4	8.2	3	3	PT0571	T-cell receptor be	676	4	8.2	6	4	I79564	hypothetical TCL3
604	4	8.2	3	3	S68328	blood cell protein	677	4	8.2	7	2	A60139	fatty-acid synthas
605	4	8.2	4	2	S18401	thyroglobulin - do	678	4	8.2	7	2	S71870	glutathione transf
606	4	8.2	4	2	A61300	22K superhelical D	679	4	8.2	7	2	S55548	mcrB protein - Esc
607	4	8.2	4	2	I40505	hypothetical prote	680	4	8.2	7	2	B39127	phosphotransferase
608	4	8.2	4	2	T46627	hypothetical prote	681	4	8.2	7	2	S38516	mabinlin II chain
609	4	8.2	4	2	A27897	glucan 1,4-alpha-g	682	4	8.2	7	2	A34818	vicilin 72K chain
610	4	8.2	4	2	S39390	myosin-light-chain	683	4	8.2	7	2	PQ0254	18K protein S507 -
611	4	8.2	4	2	I61883	protamine p1 - ora	684	4	8.2	7	2	PQ0728	unidentified 5.0/1
612	4	8.2	4	2	S43959	Ig mu chain V regi	685	4	8.2	7	2	S70335	endosperm protein,
613	4	8.2	4	2	A26209	protein-glutamine	686	4	8.2	7	2	A12016	formylglycinamide

687 4 8.2 7 2 S68004 hucolin, 75K chain
688 4 8.2 7 2 A11483 aspartate transami
689 4 8.2 7 2 P70602 T-cell receptor be
690 4 8.2 7 2 P70666 T-cell receptor be
691 4 8.2 7 2 P70655 T-cell receptor be
692 4 8.2 7 2 P70665 T-cell receptor be
693 4 8.2 7 2 P70556 T-cell receptor be
694 4 8.2 7 2 P70542 T-cell receptor be
695 4 8.2 7 2 P70543 T-cell receptor be
696 4 8.2 7 2 P70722 T-cell receptor be
697 4 8.2 7 2 P70567 T-cell receptor be
698 4 8.2 7 2 P70676 T-cell receptor be
699 4 8.2 7 2 P70688 T-cell receptor be
700 4 8.2 7 2 P70728 T-cell receptor be
701 4 8.2 7 2 P70671 T-cell receptor be
702 4 8.2 7 2 A38671 sex pheromone CAM3
703 4 8.2 7 2 A35269 peptidylglycine mo
704 4 8.2 7 2 S33567 tubulin beta-3 cha
705 4 8.2 7 2 A58512 venom heptapeptide
706 4 8.2 8 2 P4131 hypothetical prote
707 4 8.2 8 2 T10077 158K exoantigen -
708 4 8.2 8 2 B33099 Ig heavy chain CRD
709 4 8.2 8 2 P70298 Ig heavy chain CRD
710 4 8.2 8 2 P70323 phosphatidylethano
711 4 8.2 8 2 P70043 T-cell receptor al
712 4 8.2 8 2 A35768 T-cell receptor be
713 4 8.2 8 2 P70527 T-cell receptor be
714 4 8.2 8 2 P70653 T-cell receptor be
715 4 8.2 8 2 P70557 T-cell receptor be
716 4 8.2 8 2 P70554 T-cell receptor be
717 4 8.2 8 2 P70724 T-cell receptor be
718 4 8.2 8 2 P70725 T-cell receptor be
719 4 8.2 8 2 P4372 telomeric and tetr
720 4 8.2 8 2 S45651 probable Na+-trans
721 4 8.2 8 2 A59495 Vesicle associated
722 4 8.2 8 2 P00726 unidentified 4.5/4
723 4 8.2 8 2 S11078 glucose-6-phosphat
724 4 8.2 8 2 A21440 variant surface gl
725 4 8.2 8 2 JS0318 leucokinin VIII -
726 4 8.2 8 2 T13818 cytochrome oxidase
727 4 8.2 8 2 F60588 sperm-activating p
728 4 8.2 8 2 G60588 sperm-activating p
729 4 8.2 8 4 I55411 hypothetical hieto
730 4 8.2 9 2 P70002 chlorophyll a/b-bi
731 4 8.2 9 2 C36730 hutU protein - Kle
732 4 8.2 9 2 P70033 protein QA300033 -
733 4 8.2 9 2 P70225 Ig heavy chain CDR
734 4 8.2 9 2 P70315 Ig heavy chain CDR
735 4 8.2 9 2 S65865 collagen alpha 2(V
736 4 8.2 9 2 S36850 Ig heavy chain V r
737 4 8.2 9 2 P70634 T-cell receptor be
738 4 8.2 9 2 A33527 fructose-2,6-bisph
739 4 8.2 9 2 PS0253 glycine cleavage s
740 4 8.2 9 2 C57444 neuropeptide Grb-A
741 4 8.2 9 2 D44787 calliWRamide 13
742 4 8.2 9 2 F41978 calliWRamide 6 -
743 4 8.2 9 2 G41978 c-rel protein - ch
744 4 8.2 9 2 I50633 macrophage chemota
745 4 8.2 9 2 A37027 macrophage cytotox
746 4 8.2 9 2 A60427 delta sleep-induci
747 4 8.2 9 2 QDRB synaptosomal-assoc
748 3 6.1 4 2 E44823 globulin IV alpha
749 3 6.1 4 2 S09478 endoglucanase F -
750 3 6.1 4 2 I40804 alkanal monooxygen
751 3 6.1 5 2 A44955 hypothetical prote
752 3 6.1 7 2 S09652 NADH2 dehydrogenas
753 3 6.1 7 2 T09512 protein kinase Ci
754 3 6.1 7 2 A59489 triacylglycerol li
755 3 6.1 7 2 S5274 trichodecenen I -
756 3 6.1 7 4 PC2056 Na+-transporting A
757 3 6.1 8 2 S66296 telomeric and tetr
758 3 6.1 8 2 PC4373 R-phycoerythrin al
759 2 4.1 3 3 A22565

760 2 4.1 5 2 P00689 photosystem I 10.4
761 2 4.1 5 2 B61445 leu-enkephalin - b
762 2 4.1 5 2 A61445 Met-enkephalin - b
763 2 4.1 6 2 B44510 hypothetical prote
764 2 4.1 6 2 B35640 cerebellar degener
765 2 4.1 7 2 A60224 Met-enkephalin-Arg
766 2 4.1 7 2 P00012 cholecystokinin -
767 2 4.1 8 2 A43001 cholecystokinin -
768 2 4.1 9 2 P70108 late GI-69 protein
769 1 2.0 3 3 S13894 histidinol dehydro
770 1 2.0 3 3 B23751 spinal cord peptid
771 1 2.0 4 2 D41654 hypothetical prote
772 1 2.0 4 2 I40870 phospholipase C (E
773 1 2.0 4 2 A53284 T-cell receptor be
774 1 2.0 4 2 B3284 T-cell receptor be
775 1 2.0 4 2 S47552 ubiquitin - rat
776 1 2.0 4 2 A60418 FMRFamide - polych
777 1 2.0 4 2 ECNK cardioexcitatory n
778 1 2.0 5 2 A32516 cholecystokinin-5
779 1 2.0 5 2 B45525 actin I - malaria
780 1 2.0 6 2 B33932 Ig mu chain D regi
781 1 2.0 7 4 PC2057 trichodecenen II -
782 1 2.0 9 2 PH0942 T-cell receptor be
783 0 0.0 3 3 E37196 bradykinin-potenti
784 0 0.0 3 3 E37196 bradykinin-potenti
785 0 0.0 3 3 A23751 spinal cord peptid
786 0 0.0 4 1 ECKAA ancho-RFamide neu
787 0 0.0 4 2 A25844 auto-RF amide neu
788 0 0.0 4 2 S5238 pallidipin - assas
789 0 0.0 5 2 A33882 cadmium-binding pe
790 0 0.0 5 2 S65726 hemoglobin, extrac
791 0 0.0 7 2 B33882 cadmium-binding he

ALIGNMENTS

RESULT 1

B39745 endoglycosylceramidase (BC 3.2.1.123) I - Rhodococcus sp. (fragment)

C:Species: Rhodococcus sp.

C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 31-Dec-1993

C:Accession: B39745

R:Ito, M.; Ikegami, Y.; Yamagata, T.

J. Biol. Chem. 266, 7919-7926, 1991

A:Title: Activator proteins for glycosphingolipid hydrolysis by endoglycosylceramidases. E.I.

ble using these activator proteins.

A:Reference number: A39745; MUID:91210321; PMID:1850427

A:Accession: B39745

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <ITO>

C:Cross-references: UNIPARC:UPI000017AD78

C:Keywords: glycosidase; hydrolase

Query Match 36.7%; Score 18; DB 2; Length 8;

Best Local Similarity 100.0%; Pred.No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 APP 5

Db 1 APP 3

RESULT 2

B41983

orf dowstream to bacterioferritin - Azotobacter vinelandii (fragment)

C:Species: Azotobacter vinelandii

C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: B41983

R:Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, E.I.

Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992

A:Title: Unification of the ferritin family of proteins.

A:Reference number: A41983; MUID:92196129; PMID:1549605
 A:Accession: B41983
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid; protein
 A:Residues: 1-9 <GRO>
 A:Cross-references: UNIPROT:P25825; UNIPARC:UPI000013A327; GB:M83692; NID:gl42297; PIDN:
 A:Note: sequence extracted from NCBI backbone (NCBI:P88442)

Query Match 36.7%; Score 18; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 APP 5
 Db 2 APP 4

RESULT 3

B37988
 acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
 C:Species: Physarum polycephalum
 C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
 A:Accession: B37988
 R:Murakami-Murofuehi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Og
 J. Biol. Chem. 265, 1998-19903, 1990
 A:Title: Purification and characterization of a novel intracellular acid proteinase from
 A:Reference number: A37988; MUID:91060508; PMID:2246266
 A:Accession: B37988
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <MUR>
 A:Cross-references: UNIPARC:UPI000017B19F

Query Match 34.7%; Score 17; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPV 6
 Db 3 PPI 5

RESULT 4

PC7078
 unidentified 48.7K protein - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
 A:Accession: PC7078
 R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
 Electrophoresis 21, 1853-1871, 2000
 A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of b
 A:Reference number: PC7078
 A:Accession: PC7078
 A:Molecule type: protein
 A:Residues: 1-9 <TSU>
 A:Cross-references: UNIPROT:Q91YTO; UNIPARC:UPI000017C882
 A:Experimental source: strain C57BL/6Cr Slc, male; brain, striatum
 C:Keywords: brain

Query Match 34.7%; Score 17; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAP 4
 Db 4 TTAP 7

RESULT 5

E61491
 seed protein wa-5 - winged bean (fragment)
 C:Species: Psophocarpus tetragonolobus (winged bean)
 C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C:Accession: E61491

R: Hirano, H.
 J. Protein Chem. 8, 115-130, 1989
 A:Title: Microsequence analysis of winged bean seed proteins electroblooded from two-di
 A:Reference number: A61491; MUID:89351606; PMID:2765119
 A:Accession: E61491
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <HIR>
 A:Cross-references: UNIPARC:UPI000017B074
 C:Keywords: glycoprotein; seed

Query Match 32.7%; Score 16; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STAP 4
 Db 1 STVP 4

RESULT 6

PT0530
 T-cell receptor beta chain V-D-J region (100-4AK) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 A:Accession: PT0530
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0530
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-8 <FEE>
 A:Cross-references: UNIPARC:UPI000017C7BB
 A:Experimental source: adult thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 32.7%; Score 16; DB 2; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAP 4
 Db 2 SSAP 5

RESULT 7

PT0559
 T-cell receptor beta chain V-D-J region (126-1BH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 A:Accession: PT0559
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0559
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-8 <FEE>
 A:Cross-references: UNIPARC:UPI000017C80E
 A:Experimental source: day 18 fetal thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 32.7%; Score 16; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STAP 5
 Db 1 ASGPP 5

RESULT 8

S43971
tumor-associated antigen MUT1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 16-Aug-2004
C:Accession: S43971
R:Mandelblat, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.
Nature 369, 67-71, 1994
A:Title: CTL induction by a tumour-associated antigen octapeptide derived from a murine
A:Reference number: S43971; MUID:94217811; PMID:8164742
A:Accession: S43971
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <MAN>
A:Cross-references: UNIPROT:Q7M067; UNIPARC:UPI000017A4FF

Query Match 32.7%; Score 16; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STAPP 5
: || |
DB 4 NTAQP 8

RESULT 9

S21288
lectin - potato (fragment)
C:Species: Solanum tuberosum (potato)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C:Accession: S21288
R:Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
Biochem. J. 283, 813-821, 1992
A:Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterization
A:Reference number: S21288; MUID:92272683; PMID:1590771
A:Accession: S21288
A:Molecule type: protein
A:Residues: 1-8 <MIL>
A:Cross-references: UNIPROT:Q7M1V6; UNIPARC:UPI000017B0BF
A:Experimental source: var. Ulster Sceptre
C:Function:
A:Description: may be involved in defence mechanism of the plant
C:Keywords: hydroxyproline; lectin

Query Match 30.6%; Score 15; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 APP 5
: || |
DB 6 SPP 8

RESULT 10

A31570
angiotensin-converting enzyme inhibitor - yellowfin tuna
C:Species: Thunnus albacares (yellowfin tuna)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 05-Oct-2004
C:Accession: A31570
R:Kohama, Y.; Matsumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.
Biochem. Biophys. Res. Commun. 155, 332-337, 1988
A:Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.
A:Reference number: A31570; MUID:88326322; PMID:3415688
A:Accession: A31570
A:Molecule type: protein
A:Residues: 1-8 <KOH>
A:Cross-references: UNIPROT:P18691; UNIPARC:UPI0000035267
A:Note: the source is designated as Neothunnus macropterus
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 30.6%; Score 15; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PVH 7
: || |
DB 1 PTH 3

RESULT 11

B30572
T-cell receptor beta chain C region (CRTB29) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997
C:Accession: B30572
R:Williams, C.B.; Gutman, G.A.
J. Immunol. 142, 1027-1035, 1989
A:Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utilization
A:Reference number: A30563; MUID:89110038; PMID:2563271
A:Accession: B30572
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-9 <WIL>
A:Cross-references: UNIPARC:UPI000017C9D5
C:Keywords: T-cell receptor

Query Match 30.6%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STAPP 5
: || |
DB 5 TVTPP 9

RESULT 12

S55696
phosphoenolpyruvate carboxykinase - Trypanosoma brucei
C:Species: Trypanosoma brucei
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S55696
R:Hunt, M.; Koehler, P.
Biochim. Biophys. Acta 1249, 15-22, 1995
A:Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Try
A:Reference number: S55696; MUID:95284106; PMID:7766679
A:Accession: S55696
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <HUN>
A:Cross-references: UNIPROT:Q7M3S5; UNIPARC:UPI000017B599

Query Match 30.6%; Score 15; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PPVH 7
: || |
DB 2 PIH 5

RESULT 13

PQ0727
H2 class I protein [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PQ0727
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A:Reference number: PQ0696
A:Accession: PQ0727
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <KOM>

A;Cross-references: UNIPARC:UPI000017B10C

Query Match 28.6%; Score 14; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APPV 6
|||
DB 2 APV 5

RESULT 14

S71299
ICL2 protein - Paramecium tetraurelia (fragment)

C;Species: Paramecium tetraurelia

C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999

C;Accession: S71299

R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.

Eur. J. Biochem. 238, 121-128, 1996

A;Title: Characterization of centrln genes in Paramecium.

A;Reference number: S71298; MUID:96248429; PMID:8665928

C;Accession: S71299

A;Molecule type: protein

A;Residues: 1-7 <HAD>

A;Cross-references: UNIPARC:UPI000017B66B

A;Experimental source: strain d4-2

C;Genetics:

A;Genetic code: SGC5

Query Match 28.6%; Score 14; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
|||
DB 3 PP 4

RESULT 15

S09027

carboxylesterase (EC 3.1.1.1) MK2, microsomal - crab-eating macaque (fragment)

C;Species: Macaca fascicularis (Crab-eating macaque)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Apr-1993

C;Accession: S09027

R;Hosokawa, M.; Maki, T.; Satoh, T.

Arch. Biochem. Biophys. 277, 219-227, 1990

A;Title: Characterization of molecular species of liver microsomal carboxylesterases of

A;Reference number: S09021; MUID:90179180; PMID:2310190

C;Accession: S09027

A;Molecule type: protein

A;Residues: 1-7 <HOS>

A;Cross-references: UNIPARC:UPI000017C058

C;Keywords: carboxylic ester hydrolase

Query Match 28.6%; Score 14; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STAPPV 6
|||
DB 2 SASPV 7

RESULT 16

PT0283

Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0283

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and f

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0283

A;Molecule type: DNA

A;Residues: 1-7 <YAM>

A;Cross-references: UNIPARC:UPI000017C206

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 14; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
|||
DB 6 PP 7

RESULT 17

A61081

tryptophyllin, basic - Rohde's leaf frog

C;Species: Phyllomedusa rohdei (Rohde's leaf frog)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004

C;Accession: A61081

R;Montecucchi, P.C.; Vincenti, M.; Lazarini, A.M.; Rusconi, L.; Erspamer, V.

Int. J. Pept. Protein Res. 33, 391-395, 1989

A;Title: Isolation, structure determination and synthesis of a novel tryptophan-containing

A;Reference number: A61081

C;Accession: A61081

A;Molecule type: protein

A;Residues: 1-7 <MON>

A;Cross-references: UNIPARC:UPI000002C690

C;Comment: The biological activity of this peptide was not determined.

C;Keywords: amidated carboxyl end; hydroxyproline; skin

F;3/Modified site: 4-hydroxyproline (Pro) #status experimental

F;7/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.6%; Score 14; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
|||
DB 2 PP 3

RESULT 18

S16324

hypothetical protein 2 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000

C;Accession: S16324

R;Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.

EMBO J. 10, 1787-1791, 1991

A;Title: A novel class of plant proteins containing a homeodomain with a closely linked

A;Reference number: S16323; MUID:91266907; PMID:1675603

C;Accession: S16324

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-8 <RUB>

A;Cross-references: UNIPARC:UPI0000011DF52; EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID

Query Match 28.6%; Score 14; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
|||
DB 7 PP 8

RESULT 19

S10783

enamelin f - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998

C;Accession: S10783

R;Strawich, E.; Glimcher, M.J.

Eur. J. Biochem. 191, 47-56, 1990

A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albumin

A;Reference number: S10780; MUID:90336641; PMID:2379503

C;Accession: S10783

A;Molecule type: protein

A;Residues: 1-8 <STR>

A;Cross-references: UNIPARC:UPI000017C505

C;Keywords: enamel; phosphoprotein

Query Match 28.6%; Score 14; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5

||

Db 4 PP 5

RESULT 20

E47393

neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)

C;Species: Calliphora vomitoria

C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: E47393

R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.

Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993

A;Title: Callatostatins: neuropeptides from the blowfly Calliphora vomitoria with sequen

A;Reference number: A47393; MUID:93211980; PMID:8460157

A;Accession: E47393

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-8 <DUV>

A;Cross-references: UNIPROT:P41841; UNIPARC:UPI000002EAB5

A;Experimental source: whole flies

A;Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 28.6%; Score 14; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5

||

Db 2 PP 3

RESULT 21

S65433

bradykinin - horn fly (fragment)

C;Species: Haematobia irritans (horn fly)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C;Accession: S65433

R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, E

Eur. J. Biochem. 237, 414-423, 1996

A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran

A;Reference number: S65431; MUID:96215437; PMID:8647080

A;Accession: S65433

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <WIJ>

A;Cross-references: UNIPARC:UPI000002CF4A

A;Note: the source is designated as Haematobia irritans exigua

Query Match 28.6%; Score 14; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5

||

Db 2 PP 3

RESULT 22

B38740

Ig kappa chain C region (PY20) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998

C;Accession: B38740

R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991

A;Title: Heavy and light chain variable region sequences and antibody properties of anti

A;Reference number: A38740; MUID:91177923; PMID:1706720

A;Accession: B38740

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-9 <RUF>

A;Cross-references: UNIPARC:UPI0000017C6D4

Query Match 28.6%; Score 14; DB 2; Length 9;

Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 APPV 6

|||

Db 4 APTV 7

RESULT 23

S26508

collagen alpha 2(VI) chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S26508

R;Jander, R.; Rautenberg, J.; Glanville, R.W.

Eur. J. Biochem. 133, 39-46, 1983

A;Title: Further characterization of the three polypeptide chains of bovine and human sh

A;Reference number: S26506; MUID:83209648; PMID:6852033

A;Accession: S26508

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <JAN>

A;Cross-references: UNIPROT:Q7M2M9; UNIPARC:UPI0000017C4E6

C;Keywords: hydroxyproline

F;7/Modified site: hydroxyproline (Pro) #status experimental

Query Match 28.6%; Score 14; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5

||

Db 6 PP 7

RESULT 24

A43065

hydroxyproline-3-bradykinin - frog (Heleophryne purcelli)

C;Species: Heleophryne purcelli

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C;Accession: A43065

R;Nakajima, T.; Yasuhara, T.; Erspamer, G.F.; Visser, J.

Experientia 35, 1133, 1979

A;Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of the South A

A;Reference number: A43065; MUID:80024576; PMID:488255

A;Accession: A43065

A;Molecule type: protein

A;Residues: 1-9 <NAK>

A;Cross-references: UNIPROT:Q7LZ17; UNIPARC:UPI000002CF4A

C;Keywords: bradykinin; hydroxyproline; skin

F;3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 28.6%; Score 14; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
||
Db 2 PP 3

RESULT 25
PC7073
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: PC7073
R:Tsuigita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of b
A:Reference number: PC7072
A:Accession: PC7073
A:Molecule type: protein
A:Residues: 1-9 <TSU>
A:Cross-references: UNIPROT:Q9CVK7; UNIPARC:UPI000017CDB7
C:Keywords: brain; core protein; oxidoreductase

Query Match 28.6%; Score 14; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 APPV 6
||
Db 5 APKV 8

RESULT 26
B60246
ornitho-kinin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 16-Aug-2004
C:Accession: B60246
R:Kimura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.
Adv. Exp. Med. Biol. 247A, 359-367, 1989
A:Title: Ornitho-kininogen and ornitho-kinin: isolation, characterization and chemical e
A:Reference number: A60246; MUID:90102072; PMID:2603803
A:Accession: B60246
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <KIM>
A:Cross-references: UNIPROT:Q7L250; UNIPARC:UPI000017A4F8

Query Match 28.6%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
||
Db 2 PP 3

RESULT 27
A26744
bradykinin-like peptide - garden dagger wasp
N:Alternate names: Thr-6-bradykinin
C:Species: Megascolia flavifrons (garden dagger wasp)
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004
C:Accession: A26744
R:Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.
Toxicol 25, 527-535, 1987
A:Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp
A:Reference number: A94322; MUID:87293024; PMID:3617088
A:Accession: A26744
A:Molecule type: protein
A:Residues: 1-9 <YAS>
A:Cross-references: UNIPARC:UPI000012DF29

Query Match 28.6%; Score 14; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
||
Db 2 PP 3

RESULT 28
A61057
Thr-6 bradykinin - scoliid wasp (Colpa interrupta)
C:Species: Colpa interrupta
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Oct-2004
C:Accession: A61057
R:Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Pelhate, M.; Yasuhara, T.
Comp. Biochem. Physiol. C 96, 157-162, 1990
A:Title: Threonine(6)-bradykinin in the venom of the wasp Colpa interrupta (F.) presynaf
A:Reference number: A61057; MUID:91130217; PMID:1980872
A:Accession: A61057
A:Molecule type: protein
A:Residues: 1-9 <PIE>
A:Cross-references: UNIPARC:UPI000012DF29
C:Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 28.6%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
||
Db 2 PP 3

RESULT 29
A60579
bradykinin-like peptide - slider turtle
C:Species: Pseudemys scripta (slider)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Oct-2004
C:Accession: A60579
R:Conlon, J.M.; Hicks, J.W.; Smith, D.D.
Endocrinology 126, 985-991, 1990
A:Title: Isolation and biological activity of a novel kinin ((Thr(6))bradykinin) from th
A:Reference number: A60579; MUID:90126625; PMID:2298179
A:Accession: A60579
A:Molecule type: protein
A:Residues: 1-9 <CON>
A:Cross-references: UNIPARC:UPI000012DF29
C:Comment: This peptide increases aortic blood flow but, unlike bradykinin in mammalian
C:Keywords: plasma

Query Match 28.6%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PP 5
||
Db 2 PP 3

RESULT 30
A61363
bradykinin - common frog
C:Species: Rana temporaria (common frog)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C:Accession: A61363
R:Anastasi, A.; Erspamer, V.; Bertaccini, G.
Comp. Biochem. Physiol. A 14, 43-52, 1965
A:Title: Occurrence of bradykinin in the skin of Rana temporaria.
A:Reference number: A61363
A:Accession: A61363
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <ANA>

A;Cross-references: UNIPROT:Q7LZJ8; UNIPARC:UPI0000002CF4A
C;Keywords: skin

Query Match 28.6%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
||
Db 2 PP 3

RESULT 31

A61358

bradykinin-like peptide I - Japanese pond frog

C;Species: Rana nigromaculata (Japanese pond frog)

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004

C;Accession: A61358

R;Nakajima, T.

Chem.Pharm. Bull. 16, 769-770, 1968

A;Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the skin

A;Reference number: A61358; MUID:68412013; PMID:5677638

A;Accession: A61358

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <NAK>

A;Cross-references: UNIPROT:Q7LZ54; UNIPARC:UPI000017A4F0

C;Keywords: skin

Query Match 28.6%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
||
Db 2 PP 3

RESULT 32

S15595

orf 2 rara 5'-region - human

C;Species: Homo sapiens (man)

C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999

C;Accession: S15595

R;Brand, N.J.; Petkovich, M.; Chambon, P.

Nucleic Acids Res. 18, 6799-6806, 1990

A;Title: Characterization of a functional promoter for the human retinoic acid receptor-

A;Reference number: S15594; MUID:91088249; PMID:2175878

A;Accession: S15595

A;Molecule type: DNA

A;Residues: 1-9 <BRA>

A;Cross-references: UNIPARC:UPI000017CBEF; EMBL:X56057; NID:g35875

A;Note: This ORF from Fig. 2 is not annotated in GenBank entry HSRARAL, release 111.0

C;Comment: This sequence is not thought to be translated.

C;Genetics:

A;Gene: GDB:RARA

A;Cross-references: GDB:120337; OMIM:180240

A;Map position: 17q12-17q12

Query Match 28.6%; Score 14; DB 4; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STAPP 5
|||
Db 4 STRAP 8

RESULT 33

A44916

mosquitocidal toxin 21 - Bacillus sphaericus (fragment)

C;Species: Bacillus sphaericus

C;Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995

C;Accession: A44916
R;Thanabalu, T.; Hindley, J.; Berry, C.

J. Bacteriol. 174, 5051-5056, 1992

A;Title: Proteolytic processing of the mosquitocidal toxin from Bacillus sphaericus SSII

A;Reference number: A44916; MUID:92332441; PMID:1352768

C;Accession: A44916

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-6 <THA>

A;Cross-references: UNIPARC:UPI000017ACA7

A;Experimental source: SSII-1

A;Note: sequence extracted from NCBI backbone (NCBIP:108973)

Query Match 26.5%; Score 13; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 STAPP 5
|||
Db 1 SMASP 5

RESULT 34

PT0654

T-cell receptor beta chain V-D-J region (121-1BK) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0654

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0654

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <PEE>

A;Cross-references: UNIPARC:UPI000017C7EA

A;Experimental source: day 4 postnatal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 26.5%; Score 13; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STAP 4
|||
Db 2 SGAP 5

RESULT 35

A15398

choline oxidase (EC 1.1.3.17) - Alcaligenes sp. (tentative sequence) (fragment)

C;Species: Alcaligenes sp.

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004

C;Accession: A15398

R;Ohka-Fukuyama, M.; Miyake, Y.; Emi, S.; Yamano, T.

J. Biochem. 88, 197-203, 1980

A;Title: Identification and properties of the prosthetic group of choline oxidase from A

A;Reference number: A15398; MUID:81006769; PMID:6997283

A;Accession: A15398

A;Molecule type: protein

A;Residues: 1-7 <OHT>

A;Cross-references: UNIPROT:P16101; UNIPARC:UPI00001278AA

C;Keywords: oxidoreductase

Query Match 26.5%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PVNH 8
|||
Db 3 PNHS 6

RESULT 36
A58725
virotoxin - destroying angel
C:Species: Amanita virosa (destroying angel)
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: A58725
R:Faulstich, H.; Buku, A.; Bodenmueller, H.; Wieland, T.
Biochemistry 19, 334-343, 1980
A>Title: Virotoxins: actin-binding cyclic peptides of Amanita virosa mushrooms.
A:Reference number: A58725; MUID:6893271; PMID:6893271
A:Accession: A58725
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <FAU>
A:Cross-references: UNIPARC:UPI000017CF29
C:Keywords: D-amino acid; hydroxyproline; toxin; unencoded polypeptide
F:1-7/Cross-link: cyclopeptide (Val-Leu) #status experimental
F:2/Modified site: D-threonine (Thr) #status experimental
F:3/Modified site: D-serine (Ser) #status experimental
F:4/Modified site: (3R,4S)-3,4-dihydroxyproline (Pro) #status experimental
F:6/Modified site: 2'-methylsulfonyltryptophan (Trp) #status experimental
F:7/Modified site: 4,5-dihydroxyisoleucine (Leu) #status experimental

Query Match 26.5%; Score 13; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAP 4
:|
Db 2 TSP 4

RESULT 37
A37832
phenol 2-monooxygenase (EC 1.14.13.7) chain P5 - Pseudomonas sp. (strain CF600) (fragment)
C:Species: Pseudomonas sp.
C>Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 23-Jun-1993
C:Accession: A37832
R:Powlowski, J.; Shingler, V. 1990
J. Bacteriol. 172, 6834-6840, 1990
A>Title: In vitro analysis of polypeptide requirements of multicomponent phenol hydroxylase
A:Reference number: A37832; MUID:91072231; PMID:2254259
A:Accession: A37832
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <POW>
A:Cross-references: UNIPARC:UPI000017A9A5
C:Keywords: oxidoreductase

Query Match 24.5%; Score 12; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 HNV 9
:|
Db 2 YNV 4

RESULT 38
T10954
hypothetical protein 3 - spring vetch
C:Species: Vicia sativa (spring vetch)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: T10954
R:Christiansen, A.; Hansen, A.C.; Vijn, I.; Pallisgard, N.; Larsen, K.; Yang, W.C.; Bisse
submitted to the EMBL Data Library, December 1995
A:Description: A novel type of DNA binding protein interacts with a conserved sequence i
A:Reference number: Z17228
A:Accession: T10954
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-5 <CHR>

A:Cross-references: UNIPARC:UPI000011B9CD; EMBL:X95995; NID:g1360633; PID:e225862

Query Match 24.5%; Score 12; DB 2; Length 5;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 VHN 8
:|
Db 3 IHS 5

RESULT 39
JS0319
subesophageal ganglion pentapeptide - house cricket
C:Species: Acheta domesticus (house cricket)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: JS0319
R:Wicker, C.; Wicker, C.
Comp. Biochem. Physiol. C 88, 185-187, 1987
A>Title: Isolation and structure of a peptide isolated from the subesophageal ganglion
A:Reference number: JS0319
A:Accession: JS0319
A:Molecule type: protein
A:Residues: 1-5 <WIC>
A:Cross-references: UNIPROT:P19991; UNIPARC:UPI00001361CE

Query Match 24.5%; Score 12; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STAP 4
:|
Db 1 AAP 4

RESULT 40
I51317
BHLH transcription factor inhibitor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51317
R:Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G.
Mech. Dev. 50, 119-130, 1995
A>Title: Id gene activity during Xenopus embryogenesis.
A:Reference number: I51316; MUID:95344988; PMID:7619724
A:Accession: I51317
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-6 <ZHA>
A:Cross-references: UNIPARC:UPI000011EA87; GB:S79038; NID:g1042006; PIDN:AAD14294.1; PID
C:Genetics:
A:Gene: XID1b

Query Match 24.5%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STAP 4
:|
Db 2 ATEP 5

RESULT 41
PT0280
Ig heavy chain CRD3 region (clone 4-91B) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0280
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0280

A:Molecule type: DNA
A:Residues: 1-6 <YAM>
A:Cross-references: UNIPARC:UPI000017C204
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 24.5%; Score 12; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TAP 4
|:
Db 4 SAP 6

RESULT 42

PC1316
large granule L3 chain - horseshoe crab (Tachypleus tridentatus) (fragment)
C:Species: Tachypleus tridentatus
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: PC1316
R:Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa
J. Biochem. 114, 307-316, 1993
A:Title: Separation of large and small granules from horseshoe crab (Tachypleus tridentatus)
A:Reference number: PC1309; MUID:94110249; PMID:8282718
A:Accession: PC1316
A:Molecule type: protein
A:Residues: 1-7 <SHI>
A:Cross-references: UNIPARC:UPI000017BDFA
C:Comment: This protein participates in immobilization of invading microbes.

Query Match 24.5%; Score 12; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TAPP 5
|:
Db 1 TSQP 4

RESULT 43

PT0246
Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0246
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0246
A:Molecule type: DNA
A:Residues: 1-7 <YAM>
A:Cross-references: UNIPARC:UPI000017C1E5
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 24.5%; Score 12; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 HNV 9
|:
Db 1 HEV 3

RESULT 44

S66419
tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)
C:Species: Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 31-Dec-2004
C:Accession: S66419
R:Kuwabara, T.

FEBS Lett. 371, 195-198, 1995

A:Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of spinacia oleracea
A:Reference number: S66419; MUID:95402209; PMID:7672127
A:Accession: S66419
A:Molecule type: protein
A:Residues: 1-9 <KUM>
A:Cross-references: UNIPROT:Q9T2K8; UNIPROT:Q41388; UNIPARC:UPI000017AF31
C:Superfamily: polyphenol oxidase, plant type

Query Match 24.5%; Score 12; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 APPVHNV 9
|:
Db 1 APILPDV 7

RESULT 45

SI3889
phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize
C:Species: Zea mays (maize)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
C:Accession: SI3889
R:Jiao, J.; Chollet, R.
Arch. Biochem. Biophys. 283, 300-305, 1990
A:Title: Regulatory phosphorylation of serine-15 in maize phosphoenolpyruvate carboxylase
A:Reference number: SI3889; MUID:91112741; PMID:2148863
A:Accession: SI3889
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <JIA>
A:Cross-references: UNIPROT:Q43267; UNIPROT:Q41197; UNIPARC:UPI000017B168
C:Superfamily: phosphoenolpyruvate carboxylase
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 24.5%; Score 12; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 HNV 9
|:
Db 2 HSI 4

RESULT 46

S70332
endosperm protein, 10K - rye (fragment)
C:Species: Secale cereale (rye)
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C:Accession: S70332
R:Roche, A.; Calero, M.; Soriano, F.; Mendez, E.
Biochim. Biophys. Acta 1295, 13-22, 1996
A:Title: Identification of major rye secalins as coeliac immunoreactive proteins.
A:Reference number: S70327; MUID:96283789; PMID:8679669
A:Accession: S70332
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <ROC>
A:Cross-references: UNIPARC:UPI000017B132

Query Match 24.5%; Score 12; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TAP 4
|:
Db 1 TGP 3

RESULT 47

PT0247
Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0247
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0247
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Cross-references: UNIPARC:UPI000017C1E6
A;Experimental source: B lymphocyte
C;Keywords: heterotrimer; immunoglobulin

Query Match 24.5%; Score 12; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TAP 4
|||
Db 2 SAP 4

RESULT 48
PL0139
carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydoflava (fr
C;Species: Pseudomonas carboxydoflava
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: PL0139
R;Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrog
A;Reference number: PL0138; MUID:90055678; PMID:2818128
A;Accession: PL0139
A;Molecule type: protein
A;Residues: 1-9 <KRA>
A;Cross-references: UNIPROT:P1913; UNIPARC:UPI000017A976
A;Note: 2-Met is also found
C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me
C;Keywords: oxidoreductase

Query Match 24.5%; Score 12; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PVHN 8
|||
Db 4 PVQD 7

RESULT 49
SI0920
venom protein HR-3 - oriental hornet (fragment)
C;Species: Vespa orientalis (oriental hornet)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C;Accession: SI0920
R;Tsuchibaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
Biochemistry (N.Y.) 53, 183-190, 1988
A;Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. S
A;Reference number: S06445
A;Accession: SI0920
A;Molecule type: protein
A;Residues: 1-9 <TUI>
A;Cross-references: UNIPROT:Q7M471; UNIPARC:UPI000017BF07
C;Keywords: venom

Query Match 24.5%; Score 12; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VH 7
|||
Db 3 VH 4

RESULT 50
AS6029
N-methylpurine DNA glycosylase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: AS6029
R;ROY, R.; Brooks, C.; Mitra, S.
Biochemistry 33, 15131-15140, 1994
A;Title: Purification and biochemical characterization of recombinant N-methylpurine-DNA
A;Reference number: AS6029; MUID:95092772; PMID:7999773
A;Accession: AS6029
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <ROY>
A;Cross-references: UNIPROT:Q7M0H1; UNIPARC:UPI000017C703

Query Match 24.5%; Score 12; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 HNV 9
|||
Db 3 HEV 5

Search completed: February 24, 2006, 10:18:41
Job time : 42 secs

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GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: February 24, 2006, 10:10:41 ; Search time 181 Seconds
 (without alignments)
 21.848 Million cell updates/sec

Title: US-10-019-513-1
 Perfect score: 49
 Sequence: 1 STAPPVHV 9

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 401289

Minimum DB seq length: 0
 Maximum DB seq length: 9

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_21:*

1: Geneseqp1980s:*	2: Geneseqp1990s:*	3: Geneseqp2000s:*	4: Geneseqp2001s:*	5: Geneseqp2002s:*	6: Geneseqp2003as:*	7: Geneseqp2003bs:*	8: Geneseqp2004s:*	9: Geneseqp2005s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	4	AAB11114 Human MUC
2	49	100.0	9	5	ABG79089 Human MUC
3	49	100.0	9	6	ADA50588 Mucin 1 (
4	49	100.0	9	8	ADG89655 Class I H
5	49	100.0	9	8	ADG89655 Antigenic
6	49	100.0	9	8	ADG20359 Human MUC
7	49	100.0	9	8	ADU49630 Human MUC
8	49	100.0	9	9	ADX08605 Class I H
9	39	79.6	9	9	ADY51475 HLA-A2 pe
10	39	79.6	9	2	AAR68013 Mucin pep
11	39	79.6	9	2	AAR78844 MUC-1 pro
12	39	79.6	9	2	AAR72715 Mucin pep
13	39	79.6	9	2	AAY46704 Immunofogen
14	39	79.6	9	3	AAR67583 T-cell ac
15	39	79.6	9	3	AAB33656 MHC class
16	39	79.6	9	4	AAR09540 Human HLA
17	39	79.6	9	4	AAR95902 MHC class
18	39	79.6	9	4	ABG93752 Human MUC
19	39	79.6	9	5	AAB86120 Human ant
20	39	79.6	9	5	ABG79088 Human MUC
21	39	79.6	9	6	AUA82062 Antigenic
22	39	79.6	9	6	ADA50590 Mucin 1 (
23	39	79.6	9	6	ABU96608 MHC class
24	39	79.6	9	8	ADG89654 Class I H
25	39	79.6	9	8	ADG87165 Genetic v

25	39	79.6	9	8	ADU49634 Human MUC
26	39	79.6	9	9	ADX08604 Class I H
27	39	79.6	9	9	ADY26204 MHC Class
28	39	79.6	9	9	ADZ66315 MUC1 repe
29	36	73.5	9	2	AAR67603 Human MUC
30	35	71.4	9	2	AAR68012 Mucin pep
31	35	71.4	9	2	AAR68014 Mucin pep
32	35	71.4	9	2	AAR68011 Mucin pep
33	35	71.4	9	2	AAR72714 Mucin pep
34	35	71.4	9	2	AAR72713 Mucin pep
35	35	71.4	9	2	AAR72716 Mucin pep
36	35	71.4	9	4	AAE09534 Human muc
37	35	71.4	9	8	ADS87178 Genetic v
38	35	71.4	9	8	ADS87177 Genetic v
39	35	71.4	9	8	ADS87166 Genetic v
40	32	65.3	8	6	ABG73822 MUC1 asso
41	31.5	64.3	8	5	AAE26804 Human HLA
42	31.5	64.3	8	5	AEA36310 Human MUC
43	31	63.3	6	2	AAW38247 Extended
44	31	63.3	6	4	AAW72482 Fusion pr
45	31	63.3	9	3	AAY82854 Mucin pep
46	31	63.3	9	4	AU00540 Human MUC
47	31	63.3	9	7	ADB84181 Human MUC
48	31	63.3	9	7	ADD88876 Human MUC
49	31	63.3	9	9	ADZ66308 MUC1 (167
50	30	61.2	8	4	AAAB31282 Antigenic
51	30	61.2	9	2	AAAR68015 Mucin pep
52	30	61.2	9	2	AAW72717 Mucin pep
53	30	61.2	9	4	AAE09569 Human muc
54	30	61.2	9	8	ADN93265 Human muc
55	30	61.2	9	8	ADN92079 Human 202
56	30	61.2	9	8	ADN92467 Human 202
57	30	61.2	9	8	ADN92389 Human 202
58	30	61.2	9	8	ADN90125 Human 202
59	30	61.2	9	8	ADN91990 Human 202
60	30	61.2	9	8	ADN93148 Human 202
61	30	61.2	9	8	ADN90452 Human 202
62	30	61.2	9	8	ADN90469 Human 202
63	30	61.2	9	8	ADN91396 Human 202
64	30	61.2	9	8	ADN89775 Human 202
65	30	61.2	9	8	ADN92860 Human 202
66	30	61.2	9	8	ADN92859 Human 202
67	30	61.2	9	8	ADN93311 Human 202
68	30	61.2	9	8	ADN90745 Human 202
69	30	61.2	9	8	ADN92236 Human 202
70	30	61.2	9	8	ADN91111 Human 202
71	30	61.2	9	8	ADS87167 Genetic v
72	28	57.1	9	2	AAAY55408 HLA bindi
73	27	55.1	6	4	AAAB72480 Fusion pr
74	27	55.1	6	4	AAAB72481 Fusion pr
75	27	55.1	9	2	AAAR68010 Mucin pep
76	27	55.1	9	2	AAW72712 Mucin pep
77	27	55.1	9	4	AAE09536 Human muc
78	27	55.1	9	4	AAU00546 Human MUC
79	27	55.1	9	8	ADS87179 Genetic v
80	27	55.1	9	8	ADS87180 Genetic v
81	26	53.1	6	2	AAAR45393 Prolyl en
82	26	53.1	6	4	AAAB72483 Fusion pr
83	26	53.1	6	4	AAAB72484 Fusion pr
84	26	53.1	7	2	AAAR09417 LFA-1 alp
85	26	53.1	7	7	ADB79589 Parapoxvi
86	26	53.1	7	7	ADB84184 Human MUC
87	26	53.1	7	7	ADP75026 Parapoxvi
88	26	53.1	7	9	ADZ66312 MUC1 repe
89	26	53.1	8	6	ABU03395 Human exp
90	26	53.1	9	2	AAAR68016 Mucin pep
91	26	53.1	9	2	AAW72718 Mucin pep
92	26	53.1	9	8	ADK04638 Hepatitis
93	26	53.1	9	8	ADN93283 Human 202
94	26	53.1	9	8	ADN87168 Genetic v
95	26	53.1	9	9	ADZ57310 Cytotoxic
96	25	51.0	8	8	ADN02491 C3b bindi
97	25	51.0	9	3	AAAY54187 HLA bindi

98	25	51.0	9	4	AAm22285	AAm22285	HIV pepti	171	24	49.0	9	8	ADs75348	Human C35
99	25	51.0	9	4	AAm22287	AAm22287	HIV pepti	172	24	49.0	9	9	ADv13361	Human pho
100	25	51.0	9	4	AAU26574	AAU26574	Human Leu	173	23	49.0	9	9	Adx83757	C35 human
101	25	51.0	9	7	ABO07325	ABO07325	Human Muc	174	23	46.9	4	7	AdC28247	Stain car
102	25	51.0	9	7	ABW00337	ABW00337	Tumour-as	175	23	46.9	4	7	AdW37010	HLA bindi
103	25	51.0	9	8	AD112136	AD112136	Human BFA	176	23	46.9	4	9	ADY56624	Carotenoi
104	25	51.0	9	8	ADU74519	ADU74519	Human RSV	177	23	46.9	5	5	ABP54763	Peptide i
105	25	51.0	9	8	ADU99307	ADU99307	BFA4 tumo	178	23	46.9	5	6	AAE34886	HIV-1 Gag
106	24	49.0	6	2	AAr95608	AAr95608	Diabetoge	179	23	46.9	5	6	ADP96510	HIV GAG p
107	24	49.0	7	2	AAr96117	AAr96117	Peptide p	180	23	46.9	5	6	ABR82402	HIV Gag p
108	24	49.0	7	2	AAr883353	AAr883353	Viral rel	181	23	46.9	5	6	ADJ92025	Transport
109	24	49.0	7	7	ABR83358	ABR83358	Viral rel	182	23	46.9	6	2	AAW25661	Conserved
110	24	49.0	7	7	ADC28005	ADC28005	Synthetic	183	23	46.9	6	2	AAW64516	Neurotoxi
111	24	49.0	7	9	ADY56374	ADY56374	Carotenoi	184	23	46.9	6	5	AAE26893	Decoy pep
112	24	49.0	8	2	AAr35856	AAr35856	Hepatitis	185	23	46.9	6	5	AAU99476	BetaAP-se
113	24	49.0	8	2	ABP20620	ABP20620	HIV A03 m	186	23	46.9	6	5	ADP54765	Peptide i
114	24	49.0	8	4	ABP20375	ABP20375	HIV A03 m	187	23	46.9	6	5	ABP96512	HIV GAG p
115	24	49.0	8	4	ABP17801	ABP17801	HIV B58 s	188	23	46.9	6	6	ABR43641	Mouse CLA
116	24	49.0	8	4	ABP17900	ABP17900	HIV B58 s	189	23	46.9	6	6	ABR82404	HIV Gag p
117	24	49.0	8	8	ADr05420	ADr05420	Savinase	190	23	46.9	6	7	ADJ92027	Transport
118	24	49.0	9	2	AAr44271	AAr44271	Residues	191	23	46.9	7	5	ADP54771	Peptide i
119	24	49.0	9	2	AAr53611	AAr53611	Opitoid pe	192	23	46.9	7	5	ADP96518	HIV GAG p
120	24	49.0	9	2	AAr97535	AAr97535	Antigenic	193	23	46.9	7	6	AAE32747	Human imm
121	24	49.0	9	2	AAy40199	AAy40199	Amino aci	194	23	46.9	7	6	AAE32746	Human imm
122	24	49.0	9	2	AAy40195	AAy40195	Amino aci	195	23	46.9	7	6	ABR82410	HIV Gag p
123	24	49.0	9	2	AAy53376	AAy53376	p53 epit	196	23	46.9	7	7	ABR83356	Viral rel
124	24	49.0	9	2	AAy53372	AAy53372	p53 epit	197	23	46.9	7	7	ABR83355	Viral rel
125	24	49.0	9	2	AAy26711	AAy26711	HLA-B7 b1	198	23	46.9	7	7	ADb79456	Parapoxvi
126	24	49.0	9	2	AAy26715	AAy26715	HLA-B8 bi	199	23	46.9	7	7	ADb79721	Parapoxvi
127	24	49.0	9	3	AAb26349	AAb26349	Human CAS	200	23	46.9	7	7	ADe11627	Ebola vir
128	24	49.0	9	4	AAU26906	AAU26906	Human Leu	201	23	46.9	7	7	ADe77779	Synthetic
129	24	49.0	9	4	ABb13019	ABb13019	Human C35	202	23	46.9	7	7	RAO23605	Colon tum
130	24	49.0	9	4	ABb13212	ABb13212	Human C35	203	23	46.9	7	7	ADJ92033	Transport
131	24	49.0	9	4	ABb14174	ABb14174	Human C35	204	23	46.9	7	8	ADP69978	Hair bind
132	24	49.0	9	4	ABb14270	ABb14270	Human C35	205	23	46.9	7	8	ADP74865	Parapoxvi
133	24	49.0	9	4	ABb13147	ABb13147	Human C35	206	23	46.9	7	8	ADP75139	Parapoxvi
134	24	49.0	9	4	ABb13643	ABb13643	Human C35	207	23	46.9	7	8	ADs14007	Thrombin
135	24	49.0	9	4	ABb12592	ABb12592	Human C35	208	23	46.9	7	8	ADU69115	Gag pepti
136	24	49.0	9	4	ABb14350	ABb14350	Human C35	209	23	46.9	7	9	ADY99994	Gag prote
137	24	49.0	9	4	ABb12497	ABb12497	Human C35	210	23	46.9	7	9	ADY55676	Hair-bind
138	24	49.0	9	4	ABb14285	ABb14285	Human C35	211	23	46.9	8	2	AAr35857	Hepatitis
139	24	49.0	9	4	ABb14015	ABb14015	Human C35	212	23	46.9	8	2	AAr77556	HIV(B35) -
140	24	49.0	9	4	ABb12977	ABb12977	Human C35	213	23	46.9	8	2	AAr70539	HIV pepti
141	24	49.0	9	4	ABb13114	ABb13114	Human C35	214	23	46.9	8	2	AAw43398	C-reactiv
142	24	49.0	9	4	ABb12642	ABb12642	Human C35	215	23	46.9	8	3	AAy66403	HLA-B35-b
143	24	49.0	9	4	ABb13238	ABb13238	Human C35	216	23	46.9	8	4	AAm99070	Vaccine r
144	24	49.0	9	4	ABb13409	ABb13409	Human C35	217	23	46.9	8	4	AAg84805	MAGE3 A24
145	24	49.0	9	4	ABb14645	ABb14645	Human C35	218	23	46.9	8	4	AAg84800	MAGE3 HLA
146	24	49.0	9	4	ABb13167	ABb13167	Human C35	219	23	46.9	8	4	ABP20519	HIV A03 m
147	24	49.0	9	4	ABb13218	ABb13218	Human C35	220	23	46.9	8	4	ABP16815	HIV B07 s
148	24	49.0	9	4	ABb13192	ABb13192	Human C35	221	23	46.9	8	4	ABP20341	HIV A03 m
149	24	49.0	9	4	ABb13976	ABb13976	Human C35	222	23	46.9	8	4	ABP17868	HIV B58 s
150	24	49.0	9	4	ABP17902	ABP17902	HIV B58 s	223	23	46.9	8	4	ABP17782	HIV B58 s
151	24	49.0	9	4	ABP22649	ABP22649	HIV A11 m	224	23	46.9	8	5	ABP54773	Peptide i
152	24	49.0	9	4	ABP20377	ABP20377	HIV A03 m	225	23	46.9	8	5	ABP54775	Peptide i
153	24	49.0	9	4	ABP11663	ABP11663	HIV A01 s	226	23	46.9	8	6	ADP96520	HIV GAG p
154	24	49.0	9	4	ADP17174	ADP17174	HIV B27 s	227	23	46.9	8	6	ADP96522	HIV GAG p
155	24	49.0	9	4	ADP15627	ADP15627	HIV A24 s	228	23	46.9	8	6	ADA50829	Ebola vir
156	24	49.0	9	4	ADP20622	ADP20622	HIV A03 m	229	23	46.9	8	6	ADA50816	Ebola vir
157	24	49.0	9	4	ADP20376	ADP20376	HIV A03 m	230	23	46.9	8	6	ADA50842	Ebola vir
158	24	49.0	9	4	ABP17802	ABP17802	HIV B58 s	231	23	46.9	8	6	ABR82412	HIV Gag p
159	24	49.0	9	4	ABP14503	ABP14503	HIV A03 s	232	23	46.9	8	6	ABR82414	HIV Gag p
160	24	49.0	9	4	ADP15629	ADP15629	HIV A24 s	233	23	46.9	8	7	ABR83354	Viral rel
161	24	49.0	9	4	ADP11661	ADP11661	HIV A01 s	234	23	46.9	8	7	ABR88774	Peyers pa
162	24	49.0	9	4	AAg77872	AAg77872	Human C35	235	23	46.9	8	7	ADC22890	E-Cadheri
163	24	49.0	9	5	AAU78533	AAU78533	Subtilisi	236	23	46.9	8	7	ADJ89091	Human her
164	24	49.0	9	6	ABR27261	ABR27261	Human can	237	23	46.9	8	7	ADJ88574	Ebola vir
165	24	49.0	9	6	ABR28182	ABR28182	Human can	238	23	46.9	8	7	ADJ88571	Ebola vir
166	24	49.0	9	6	ABR27196	ABR27196	Human can	239	23	46.9	8	7	ADJ92037	Transport
167	24	49.0	9	6	ABR27862	ABR27862	Human can	240	23	46.9	8	7	ADJ92035	Transport
168	24	49.0	9	6	ABR27977	ABR27977	Human can	241	23	46.9	8	7	ADJ88573	Ebola vir
169	24	49.0	9	6	ABR28413	ABR28413	Human can	242	23	46.9	8	7	ADJ89090	Human her
170	24	49.0	9	6	ABR27653	ABR27653	Human can	243	23	46.9	8	7	ADJ88659	Hepatitis

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245 23 46.9 8 7 ADJ89088 Human her
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247 23 46.9 8 7 ADJ88572 Ebola vir
248 23 46.9 8 7 ADJ88801 Human her
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258 23 46.9 9 2 AAR46517 HIV rever
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267 23 46.9 9 2 AAR97514 Cytotoxic
268 23 46.9 9 2 AAR45184 C-reactiv
269 23 46.9 9 2 AAR43404 C-reactiv
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381 23 46.9 9 5 ABP47460 N. mening
382 23 46.9 9 5 ABP47370 N. mening
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389 23 46.9 9 5 ABP54777 Peptide i

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392 23 46.9 9 6 ABP72152 Abp72152 Peptide e 465
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9 7 ADB67494 Adb67494 Mouse Wtl 538
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9 7 ADD96867 Add96867 HIV-1 cro 541
9 7 ADD96225 Add96225 HIV-1 cro 542
9 7 ADE77781 Ade77781 Synthetic 543
9 7 ADG38619 Adg38619 Human imm 544
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9 7 ADG38645 Adg38645 Human mel 547
9 7 ADG38737 Adg38737 Human mel 548
9 7 ADG38629 Adg38629 Human imm 549
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9 7 ADJ80727 Adj80727 Wilm's tu 551
9 7 ADJ80611 Adj80611 Wilm's tu 552
9 7 ADJ88665 Adj88665 Hepatitis 553
9 7 ADJ89096 Adj89096 Human her 554
9 7 ADJ88666 Adj88666 Hepatitis 555
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9 7 ADJ88664 Adj88664 Hepatitis 557
9 7 ADJ88808 Adj88808 Human her 558
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9 7 ADJ89095 Adj89095 Human her 560
9 7 ADJ89094 Adj89094 Human her 561
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9 7 ADJ88576 Adj88576 Ebola vir 563
9 7 ADJ89093 Adj89093 Human her 564
9 7 ADJ88806 Adj88806 Human her 565
9 7 ADJ92038 Adj92038 Transport 566
9 7 ADJ88807 Adj88807 Human her 567
9 7 ADJ92042 Adj92042 Transport 568
9 7 ADJ88578 Adj88578 Ebola vir 569
9 7 ADJ88668 Adj88668 Hepatitis 570
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9 7 ADW32159 Adw32159 HLA bindi 606
9 7 ADW32256 Adw32256 HLA bindi 607

536	23	46.9	9	7	ADW32261	Adw32261	HLA bindi	609	22	44.9	7	2	AAW79782	Proline-r
537	23	46.9	9	8	ADH97630	Ade97630	Immunogen	610	22	44.9	7	2	AAW99328	Human Igg
538	23	46.9	9	8	ADH48551	Adh48551	HIV-1 Pol	611	22	44.9	7	3	AAH17240	SH3 antag
539	23	46.9	9	8	ADJ79550	Adj79550	CTL epitope	612	22	44.9	7	3	AAV69980	Src SH3 r
540	23	46.9	9	8	ADK68777	Adk68777	Epitope 1	613	22	44.9	7	4	AAH61844	Human Iq
541	23	46.9	9	8	ADK69322	Adk69322	Epitope 1	614	22	44.9	7	5	ABB83464	Tissue In
542	23	46.9	9	8	ADK68752	Adk68752	Epitope 1	615	22	44.9	7	5	ABB83463	Tissue In
543	23	46.9	9	8	ADK69541	Adk69541	Epitope 1	616	22	44.9	7	5	ABB73233	Src homol
544	23	46.9	9	8	ADK69053	Adk69053	Epitope 1	617	22	44.9	7	6	ABP74997	Proteome
545	23	46.9	9	8	ADJ83647	Adj83647	Murine WT	618	22	44.9	7	6	AAO23192	Template-
546	23	46.9	9	8	ADJ83573	Adj83573	Human WT1	619	22	44.9	7	7	ADB79448	Parapoxvi
547	23	46.9	9	8	ADJ83531	Adj83531	Human WT1	620	22	44.9	7	7	ADJ73387	SH3 antag
548	23	46.9	9	8	ADLS7419	Adl57419	Human WT-	621	22	44.9	7	8	ADJ53021	CH1 delet
549	23	46.9	9	8	ADLS7461	Adl57461	Human WT-	622	22	44.9	7	8	ADJ51982	CH1 delet
550	23	46.9	9	8	ADLS7535	Adl57535	Mouse WT-	623	22	44.9	7	8	ADP74890	Parapoxvi
551	23	46.9	9	8	ADM73079	Adm73079	Human MAG	624	22	44.9	7	8	ADP80384	Human HLA
552	23	46.9	9	8	ADM73090	Adm73090	Human MAG	625	22	44.9	8	2	AAR84745	DYN domai
553	23	46.9	9	8	ADM73081	Adm73081	Human MAG	626	22	44.9	8	2	AAR97521	Antigenic
554	23	46.9	9	8	ADM73088	Adm73088	Human MAG	627	22	44.9	8	2	AAI40611	Al deriva
555	23	46.9	9	8	ADM97316	Adm97316	Cytotoxic	628	22	44.9	8	3	AAH29950	Scaffold
556	23	46.9	9	8	ADO09016	Ado09016	Human WT1	629	22	44.9	8	4	AAU26888	Human Leu
557	23	46.9	9	8	ADO09090	Ado09090	Mouse WT1	630	22	44.9	8	4	ABP11520	HIV A01 8
558	23	46.9	9	8	ADO08974	Ado08974	Human WT1	631	22	44.9	8	4	ABP11954	HIV A02 8
559	23	46.9	9	8	ADM63697	Adm63697	HLA bindi	632	22	44.9	8	4	AAG89703	p53 epitope
560	23	46.9	9	8	ADM63696	Adm63696	HLA bindi	633	22	44.9	8	4	AAG89580	p53 epitope
561	23	46.9	9	8	ADO24142	Ado24142	HIV epitope	634	22	44.9	8	4	AAG89526	p53 epitope
562	23	46.9	9	8	ADO23858	Ado23858	HBV pepti	635	22	44.9	8	9	ADVI2432	Human pho
563	23	46.9	9	8	ADO30651	Ado30651	Human imm	636	22	44.9	9	9	AEA14125	VEGF rela
564	23	46.9	9	8	ADQ11183	Adq11183	Synthetic	637	22	44.9	9	2	AAR44262	Residues
565	23	46.9	9	8	ADQ11403	Adq11403	Human imm	638	22	44.9	9	2	AAR44260	Residues
566	23	46.9	9	8	ADQ10851	Adq10851	Human imm	639	22	44.9	9	2	AAR59117	Peptide f
567	23	46.9	9	8	ADQ10575	Adq10575	Human imm	640	22	44.9	9	2	AAR84746	Dynamin r
568	23	46.9	9	8	ADQ10550	Adq10550	Hepatitis	641	22	44.9	9	2	AAR89165	Peptide P
569	23	46.9	9	8	ADP90883	Adp90883	HIV-1 ant	642	22	44.9	9	2	AAR97533	Antigenic
570	23	46.9	9	8	ADQ79600	Adq79600	Human Wil	643	22	44.9	9	2	AAR97510	Cytotoxic
571	23	46.9	9	8	ADR12458	Adr12458	Anti-canc	644	22	44.9	9	2	AAR97505	Cytotoxic
572	23	46.9	9	8	ADR69471	Adr69471	Novel hyb	645	22	44.9	9	2	AAW39617	Human p53
573	23	46.9	9	8	ADR69770	Adr69770	Novel hyb	646	22	44.9	9	2	AAW71346	Glycolipi
574	23	46.9	9	8	ADP79842	Adp79842	Human HLA	647	22	44.9	9	2	AAW46008	Peptide #
575	23	46.9	9	8	ADP79841	Adp79841	Human HLA	648	22	44.9	9	2	AAR78858	p53 prote
576	23	46.9	9	8	ADP79843	Adp79843	Human HLA	649	22	44.9	9	2	AAR78855	p53 prote
577	23	46.9	9	8	ADR47065	Adr47065	Control H	650	22	44.9	9	2	AAW99358	Glycosyla
578	23	46.9	9	8	ADR47127	Adr47127	Control H	651	22	44.9	9	2	AAI40182	Amino aci
579	23	46.9	9	8	ADS81055	Ads81055	Tumour-as	652	22	44.9	9	2	AAI40185	Amino aci
580	23	46.9	9	8	ADS81663	Ads81663	Tumour-as	653	22	44.9	9	2	AAI40202	Amino aci
581	23	46.9	9	8	ADS81883	Ads81883	Tumour-as	654	22	44.9	9	2	AAI47768	Immunogen
582	23	46.9	9	8	ADS81030	Ads81030	Tumour-as	655	22	44.9	9	2	AAI09158	Peptide 8
583	23	46.9	9	8	ADS81331	Ads81331	Tumour-as	656	22	44.9	9	2	AAI53359	p53 epitope
584	23	46.9	9	8	ADT74504	Adt74504	Human RSV	657	22	44.9	9	2	AAI53379	p53 epitope
585	23	46.9	9	8	ADU08007	Adu08007	Viral der	658	22	44.9	9	2	AAI53362	p53 epitope
586	23	46.9	9	8	ADT90877	Adt90877	Human imm	659	22	44.9	9	2	AAI26701	HLA-A2 bi
587	23	46.9	9	9	ADU47985	Adu47985	HLA A*020	660	22	44.9	9	2	AAI26698	HLA-A2 bi
588	23	46.9	9	9	ADV91825	Adv91825	HIV pol A	661	22	44.9	9	3	AAI33667	MHC class
589	23	46.9	9	9	ADW11940	Adw11940	Human CDI	662	22	44.9	9	3	AAI33670	MHC class
590	23	46.9	9	9	ADX39187	Adx39187	Peptide e	663	22	44.9	9	3	AAI79560	Human tum
591	23	46.9	9	9	ADX39186	Adx39186	Peptide e	664	22	44.9	9	3	AAI95884	Human MHC
592	23	46.9	9	9	ADX39190	Adx39190	Peptide e	665	22	44.9	9	3	AAI54186	HLA bindi
593	23	46.9	9	9	ADX39189	Adx39189	Peptide e	666	22	44.9	9	4	AAI22188	HIV pepti
594	23	46.9	9	9	ADX39179	Adx39179	Peptide e	667	22	44.9	9	4	AAI23294	HIV pepti
595	23	46.9	9	9	ADX39192	Adx39192	Peptide e	668	22	44.9	9	4	AAI22185	HIV pepti
596	23	46.9	9	9	ADX08751	Adx08751	HIV-CTL p	669	22	44.9	9	4	AAI95913	MHC class
597	23	46.9	9	9	ADZ37545	Adz37545	Human kin	670	22	44.9	9	4	AAI95916	MHC class
598	23	46.9	9	9	ADZ40383	Adz40383	Junctiona	671	22	44.9	9	4	AAI93763	Human p53
599	23	46.9	9	9	ADZ40567	Adz40567	Exemplary	672	22	44.9	9	4	AAI93765	Human p53
600	23	46.9	9	9	ADZ40546	Adz40546	Human leu	673	22	44.9	9	4	AAE02675	Human p53
601	23	46.9	9	9	ADZ40644	Adz40644	Multi-epi	674	22	44.9	9	4	AAE02674	Human p53
602	23	46.9	9	9	ADZ50444	Adz50444	Y. peatis	675	22	44.9	9	4	AAU06365	Human Leu
603	23	46.9	9	9	ADZ56741	Adz56741	Cytotoxic	676	22	44.9	9	4	AAE00464	Human tum
604	23	46.9	9	9	AEA39410	Aea39410	Human imm	677	22	44.9	9	4	AAE00465	Human tum
605	23	46.9	9	9	AEA26702	Aeb26702	Human imm	678	22	44.9	9	4	AAU26903	Human Leu
606	22	44.9	4	2	AAR76701	Aar76701	N-termina	679	22	44.9	9	4	AAU26573	Human Leu
607	22	44.9	5	2	AAW10818	Aaw10818	Hepatitis	680	22	44.9	9	4	ABBI3888	Human C35
608	22	44.9	7	2	AAR84747	Aar84747	GST-dynam	681	22	44.9	9	4	ABBI3605	Human C35

682	22	44.9	9	4	ABBI13868	Abbl13868 Human C35	755	22	44.9	9	7	ADW57337	Adw57337 Human 98P
683	22	44.9	9	4	ABP20245	ABP20245 HIV A03 m	756	22	44.9	9	7	ADW59146	Adw59146 Human 98P
684	22	44.9	9	4	ABP18359	ABP18359 HIV B58 s	757	22	44.9	9	7	ADW59173	Adw59173 Human 98P
685	22	44.9	9	4	ABP14097	ABP14097 HIV A02 s	758	22	44.9	9	8	ADP97579	Adp97579 Immunogen
686	22	44.9	9	4	AAg89388	Ag89388 p53 DR su	759	22	44.9	9	8	ADJ36383	Adj36383 p53 prote
687	22	44.9	9	4	AAg89521	Ag89521 p53 epito	760	22	44.9	9	8	ADJ36384	Adj36384 p53 prote
688	22	44.9	9	4	AAg89548	Ag89548 p53 epito	761	22	44.9	9	8	ADK05363	Adk05363 Hepatitis
689	22	44.9	9	4	AAg89569	Ag89569 p53 epito	762	22	44.9	9	8	ADK05386	Adk05386 Hepatitis
690	22	44.9	9	4	AAg89522	Ag89522 p53 epito	763	22	44.9	9	8	ADK03867	Adk03867 Hepatitis
691	22	44.9	9	4	AAg89522	Ag89522 p53 epito	764	22	44.9	9	8	ADK05382	Adk05382 Hepatitis
692	22	44.9	9	4	AAg89415	Ag89415 p53 DR su	765	22	44.9	9	8	ADK05385	Adk05385 Hepatitis
693	22	44.9	9	4	AAg89431	Ag89431 p53 DR su	766	22	44.9	9	8	ADK06330	Adk06330 Hepatitis
694	22	44.9	9	4	AAg89493	Ag89493 p53 DR 3a	767	22	44.9	9	8	ADK03880	Adk03880 Hepatitis
695	22	44.9	9	4	AAg89691	Ag89691 p53 epito	768	22	44.9	9	8	ADK06255	Adk06255 Hepatitis
696	22	44.9	9	4	AAg89416	Ag89416 p53 DR su	769	22	44.9	9	8	ADM57835	Adm57835 Human PBf
697	22	44.9	9	4	AAg89600	Ag89600 p53 epito	770	22	44.9	9	8	ADN91673	Adn91673 Human 202
698	22	44.9	9	5	AAW43929	Aaw43929 Human D40	771	22	44.9	9	8	ADN91350	Adn91350 Human 202
699	22	44.9	9	5	ABP47362	ABP47362 N. mening	772	22	44.9	9	8	ADN92445	Adn92445 Human 202
700	22	44.9	9	5	ABP47438	ABP47438 N. mening	773	22	44.9	9	8	ADN90134	Adn90134 Human 202
701	22	44.9	9	5	AAU95859	Aau95859 Immunogen	774	22	44.9	9	8	ADN93224	Adn93224 Human 202
702	22	44.9	9	5	ABU57363	Abu57363 p53 pepti	775	22	44.9	9	8	ADN92966	Adn92966 Human 202
703	22	44.9	9	6	ABR56430	ABr56430 p53 prote	776	22	44.9	9	8	ADS75042	AdS75042 p53 prote
704	22	44.9	9	6	ABR56429	ABr56429 p53 prote	777	22	44.9	9	8	ADV32789	Adv32789 Human 109
705	22	44.9	9	6	ABR67415	ABr67415 Human act	778	22	44.9	9	8	ADV32455	Adv32455 Human 109
706	22	44.9	9	6	ABR21583	ABr21583 Human can	779	22	44.9	9	8	ADV28003	Adv28003 Human 109
707	22	44.9	9	6	ABR22987	ABr22987 Human can	780	22	44.9	9	8	ADV32648	Adv32648 Human 109
708	22	44.9	9	6	ABR20186	ABr20186 Human can	781	22	44.9	9	8	ADV32927	Adv32927 Human 109
709	22	44.9	9	6	ABJ64631	ABj64631 184P1E2-r	782	22	44.9	9	8	ADV32822	Adv32822 Human 109
710	22	44.9	9	6	ABJ61567	ABj61567 184P1E2-r	783	22	44.9	9	8	ADU87393	Adu87393 Human tum
711	22	44.9	9	6	ABJ61139	ABj61139 184P1E2-r	784	22	44.9	9	8	ADU87394	Adu87394 Human tum
712	22	44.9	9	6	ABJ65437	ABj65437 184P1E2-r	785	22	44.9	9	9	ADU47996	Adu47996 Human p53
713	22	44.9	9	6	ABJ58854	ABj58854 184P1E2-r	786	22	44.9	9	9	ADW13795	Adw13795 Human tum
714	22	44.9	9	6	ABJ63571	ABj63571 184P1E2-r	787	22	44.9	9	9	ADM13796	Adm13796 Human tum
715	22	44.9	9	6	ABJ64076	ABj64076 184P1E2-r	788	22	44.9	9	9	ADY26215	Ady26215 MHC Class
716	22	44.9	9	6	ABJ59473	ABj59473 184P1E2-r	789	22	44.9	9	9	ADY26218	Ady26218 MHC Class
717	22	44.9	9	6	ABJ60291	ABj60291 184P1E2-r	790	22	44.9	9	9	ADZ50921	Adz50921 Y. pestis
718	22	44.9	9	6	ABJ62708	ABj62708 184P1E2-r	791	22	44.9	9	9	ADZ56791	Adz56791 Cytotoxic
719	22	44.9	9	6	ABJ62438	ABj62438 184P1E2-r	792	22	44.9	9	9	ADZ56688	Adz56688 Cytotoxic
720	22	44.9	9	6	ABR44530	ABr44530 p53 prote	793	22	44.9	9	9	ABE30757	ABe30757 p53 antiq
721	22	44.9	9	6	ABR44531	ABr44531 p53 prote	794	21	42.9	4	5	ABG32439	ABg32439 Antiviral
722	22	44.9	9	6	ABU96619	ABu96619 MHC class	795	21	42.9	4	6	AAE35851	AAe35851 Smac tetr
723	22	44.9	9	6	ABU96622	ABu96622 MHC class	796	21	42.9	4	8	ADR38576	Adr38576 Inhibitor
724	22	44.9	9	6	ABU63002	ABu63002 Human p53	797	21	42.9	5	8	ADR90645	Adr90645 Human thr
725	22	44.9	9	6	ABU63003	ABu63003 Human p53	798	21	42.9	6	2	AAW76135	Aaw76135 hML(1-6)
726	22	44.9	9	7	ADK23941	ADk23941 Human 98P	799	21	42.9	6	2	AAW73038	Aaw73038 Helicobac
727	22	44.9	9	7	ADK24848	ADk24848 Human 98P	800	21	42.9	6	9	ADZ74361	Adz74361 Human col
728	22	44.9	9	7	ADK24838	ADk24838 Human 98P	801	21	42.9	7	2	AAW76171	Aaw76171 Met-TPO(1
729	22	44.9	9	7	ADK23937	ADk23937 Human 98P	802	21	42.9	7	2	AAW76132	Aaw76132 Met-hML(1
730	22	44.9	9	7	ADW31379	ADw31379 HLA bindi	803	21	42.9	7	2	AAW76958	Aaw76958 Fusion im
731	22	44.9	9	7	ADW56662	ADw56662 Human 98P	804	21	42.9	7	8	ADS14008	AdS14008 Thrombin
732	22	44.9	9	7	ADW60033	ADw60033 Human 98P	805	21	42.9	7	8	ADS14009	AdS14009 Thrombin
733	22	44.9	9	7	ADW60045	ADw60045 Human 98P	806	21	42.9	7	8	ADT40999	Adt40999 hSARS vir
734	22	44.9	9	7	ADW55973	ADw55973 Human 98P	807	21	42.9	7	8	ADS80414	AdS80414 SARS viru
735	22	44.9	9	7	ADW60367	ADw60367 Human 98P	808	21	42.9	7	8	ADT38529	Adt38529 hSARS vir
736	22	44.9	9	7	ADW61302	ADw61302 Human 98P	809	21	42.9	7	8	ABY03567	ABy03567 SARS 1006
737	22	44.9	9	7	ADW58015	ADw58015 Human 98P	810	21	42.9	8	4	AAU26899	Aau26899 Human Leu
738	22	44.9	9	7	ADW53320	ADw53320 Human 98P	811	21	42.9	8	4	ABP12009	ABp12009 HIV A02 s
739	22	44.9	9	7	ADW56651	ADw56651 Human 98P	812	21	42.9	8	4	ABP17719	ABp17719 HIV B58 s
740	22	44.9	9	7	ADW57309	ADw57309 Human 98P	813	21	42.9	8	4	ABP17640	ABp17640 HIV B58 s
741	22	44.9	9	7	ADW57382	ADw57382 Human 98P	814	21	42.9	8	4	ABP17667	ABp17667 HIV B58 s
742	22	44.9	9	7	ADW60682	ADw60682 Human 98P	815	21	42.9	8	4	ABP12008	ABp12008 HIV A02 s
743	22	44.9	9	7	ADW55315	ADw55315 Human 98P	816	21	42.9	8	4	ABP12010	ABp12010 HIV A02 s
744	22	44.9	9	7	ADW57376	ADw57376 Human 98P	817	21	42.9	8	7	ABR62975	ABr62975 RG2 gliom
745	22	44.9	9	7	ADW61115	ADw61115 Human 98P	818	21	42.9	8	8	ADK01860	AdK01860 Hepatitis
746	22	44.9	9	7	ADW56034	ADw56034 Human 98P	819	21	42.9	8	8	ADR71476	Adr71476 Antigenic
747	22	44.9	9	7	ADW57964	ADw57964 Human 98P	820	21	42.9	8	8	ADR71569	Adr71569 SARS viru
748	22	44.9	9	7	ADW61301	ADw61301 Human 98P	821	21	42.9	8	8	ADR71567	Adr71567 SARS viru
749	22	44.9	9	7	ADW57993	ADw57993 Human 98P	822	21	42.9	8	8	ADR71568	Adr71568 SARS viru
750	22	44.9	9	7	ADW60046	ADw60046 Human 98P	823	21	42.9	8	8	ADU08135	AdU08135 Heat shoc
751	22	44.9	9	7	ADW55366	ADw55366 Human 98P	824	21	42.9	8	8	ADU04098	AdU04098 HTLV-I En
752	22	44.9	9	7	ADW59858	ADw59858 Human 98P	825	21	42.9	8	8	ADU04105	AdU04105 HTLV-I En
753	22	44.9	9	7	ADW60040	ADw60040 Human 98P	826	21	42.9	8	9	ADV12166	Adv12166 Human pho
754	22	44.9	9	7	ADW60875	ADw60875 Human 98P	827	21	42.9	8	9	ADY95906	Ady95906 SARS pept

828	21	42.9	8	9	ADY95904	Ady95904 SARS pept	901	21	42.9	9	4	AAG62107	Mouse WT1
829	21	42.9	8	9	ADY95813	Ady95813 Anti-Cdk8	902	21	42.9	9	4	AAG61974	Human WT1
830	21	42.9	8	9	ADY95905	Ady95905 SARS pept	903	21	42.9	9	4	AAG61988	Human WT1
831	21	42.9	8	9	AEA89985	Aea89985 Phage dis	904	21	42.9	9	4	ABP17035	HIV B27 s
832	21	42.9	9	2	AAr70553	AAr70553 HIV pepti	905	21	42.9	9	4	ABP18519	HIV B62 s
833	21	42.9	9	2	AAr77571	AAr77571 HIV-B51-1	906	21	42.9	9	4	ABP12157	HIV A02 s
834	21	42.9	9	2	AAW43318	AAw43318 Human leu	907	21	42.9	9	4	ABP17034	HIV B27 s
835	21	42.9	9	2	AAW49492	AAw49492 Human leu	908	21	42.9	9	4	AAU68742	Human W1
836	21	42.9	9	2	AAW49493	AAw49493 Human leu	909	21	42.9	9	4	AAU68741	Human W1
837	21	42.9	9	2	AAW49488	AAw49488 Human leu	910	21	42.9	9	4	AAU68874	Mouse W1
838	21	42.9	9	2	AAW49490	AAw49490 Human leu	911	21	42.9	9	4	AAU68755	Human W1
839	21	42.9	9	2	AAW49494	AAw49494 Human leu	912	21	42.9	9	4	AAU68740	Human W1
840	21	42.9	9	2	AAW49478	AAw49478 Human leu	913	21	42.9	9	5	ABP55704	OCIA rela
841	21	42.9	9	2	AAW49491	AAw49491 Human leu	914	21	42.9	9	5	ABP47409	N. mening
842	21	42.9	9	2	AAW49489	AAw49489 Human leu	915	21	42.9	9	5	ABP47404	N. mening
843	21	42.9	9	2	AAW07026	AAw07026 Synthetic	916	21	42.9	9	5	ABP47478	N. mening
844	21	42.9	9	2	AAW94442	AAw94442 HIV-1 gp1	917	21	42.9	9	5	ABP47372	N. mening
845	21	42.9	9	2	AAW29913	AAw29913 Porcine A	918	21	42.9	9	5	ABG33210	Human WT1
846	21	42.9	9	2	AAW47760	AAw47760 Immunogen	919	21	42.9	9	5	ABG33344	Mouse WT1
847	21	42.9	9	3	AAI98641	AAi98641 WT1 Deriv	920	21	42.9	9	5	ABG33211	Human WT1
848	21	42.9	9	3	AAI98642	AAi98642 WT1 Deriv	921	21	42.9	9	5	ABG33212	Human WT1
849	21	42.9	9	3	AAI98643	AAi98643 WT1 Deriv	922	21	42.9	9	5	ABG33225	Human WT1
850	21	42.9	9	3	AAI98775	AAi98775 WT1 Deriv	923	21	42.9	9	6	ABP85452	HLA prote
851	21	42.9	9	3	AAI98656	AAi98656 WT1 Deriv	924	21	42.9	9	6	ABP88985	HLA prote
852	21	42.9	9	3	AAI96941	AAi96941 Processed	925	21	42.9	9	6	ABP88129	HLA prote
853	21	42.9	9	4	AAW22342	AAw22342 HIV pepti	926	21	42.9	9	6	ABP88149	HLA prote
854	21	42.9	9	4	AAW22561	AAw22561 HIV pepti	927	21	42.9	9	6	ABP84846	HLA prote
855	21	42.9	9	4	AAW23229	AAw23229 HIV pepti	928	21	42.9	9	6	ABP89915	HLA prote
856	21	42.9	9	4	AAW23233	AAw23233 HIV pepti	929	21	42.9	9	6	ABP87108	HLA prote
857	21	42.9	9	4	AAW23378	AAw23378 HIV pepti	930	21	42.9	9	6	ABP87612	HLA prote
858	21	42.9	9	4	AAW22956	AAw22956 HIV pepti	931	21	42.9	9	6	ABP88757	HLA prote
859	21	42.9	9	4	AAW23379	AAw23379 HIV pepti	932	21	42.9	9	6	ABP87434	HLA prote
860	21	42.9	9	4	AAW22514	AAw22514 HIV pepti	933	21	42.9	9	6	ABP89469	HLA prote
861	21	42.9	9	4	AAW23380	AAw23380 HIV pepti	934	21	42.9	9	6	ABP86515	HLA prote
862	21	42.9	9	4	AAW22512	AAw22512 HIV pepti	935	21	42.9	9	6	ABP89324	HLA prote
863	21	42.9	9	4	AAW23239	AAw23239 HIV pepti	936	21	42.9	9	6	ABP90451	HLA prote
864	21	42.9	9	4	AAW22412	AAw22412 HIV pepti	937	21	42.9	9	6	ABP85487	HLA prote
865	21	42.9	9	4	AAW23243	AAw23243 HIV pepti	938	21	42.9	9	6	ABP88504	HLA prote
866	21	42.9	9	4	AAW23244	AAw23244 HIV pepti	939	21	42.9	9	6	ABP90521	HLA prote
867	21	42.9	9	4	AAW22413	AAw22413 HIV pepti	940	21	42.9	9	6	ABP86186	HLA prote
868	21	42.9	9	4	AAW23246	AAw23246 HIV pepti	941	21	42.9	9	6	ABP90236	HLA prote
869	21	42.9	9	4	AAW22517	AAw22517 HIV pepti	942	21	42.9	9	6	ABP87014	HLA prote
870	21	42.9	9	4	AAW22556	AAw22556 HIV pepti	943	21	42.9	9	6	ABP85155	HLA prote
871	21	42.9	9	4	AAW23241	AAw23241 HIV pepti	944	21	42.9	9	6	ABP85859	HLA prote
872	21	42.9	9	4	AAW23245	AAw23245 HIV pepti	945	21	42.9	9	6	ABP85921	HLA prote
873	21	42.9	9	4	AAW22479	AAw22479 HIV pepti	946	21	42.9	9	6	ABJ43102	151P3D4 C
874	21	42.9	9	4	AAW23232	AAw23232 HIV pepti	947	21	42.9	9	6	ABJ45935	151P3D4 C
875	21	42.9	9	4	AAW23242	AAw23242 HIV pepti	948	21	42.9	9	6	ABJ49292	151P3D4 C
876	21	42.9	9	4	AAW22516	AAw22516 HIV pepti	949	21	42.9	9	6	ABJ42402	151P3D4 C
877	21	42.9	9	4	AAW23231	AAw23231 HIV pepti	950	21	42.9	9	6	ABJ42889	151P3D4 C
878	21	42.9	9	4	AAW23234	AAw23234 HIV pepti	951	21	42.9	9	6	ABJ47032	151P3D4 C
879	21	42.9	9	4	AAW23236	AAw23236 HIV pepti	952	21	42.9	9	6	ABJ47234	151P3D4 C
880	21	42.9	9	4	AAW23238	AAw23238 HIV pepti	953	21	42.9	9	6	ABJ39380	151P3D4 C
881	21	42.9	9	4	AAW22410	AAw22410 HIV pepti	954	21	42.9	9	6	ABJ49369	151P3D4 C
882	21	42.9	9	4	AAW22558	AAw22558 HIV pepti	955	21	42.9	9	6	ABJ40228	151P3D4 C
883	21	42.9	9	4	AAW23235	AAw23235 HIV pepti	956	21	42.9	9	6	ABJ45110	151P3D4 C
884	21	42.9	9	4	AAW23237	AAw23237 HIV pepti	957	21	42.9	9	6	ABJ47898	151P3D4 C
885	21	42.9	9	4	AAW23381	AAw23381 HIV pepti	958	21	42.9	9	6	ABJ43674	151P3D4 C
886	21	42.9	9	4	AAW22411	AAw22411 HIV pepti	959	21	42.9	9	6	ABJ45228	151P3D4 C
887	21	42.9	9	4	AAW22480	AAw22480 HIV pepti	960	21	42.9	9	6	ABJ44254	151P3D4 C
888	21	42.9	9	4	AAW22557	AAw22557 HIV pepti	961	21	42.9	9	6	ABJ47871	151P3D4 C
889	21	42.9	9	4	AAW22559	AAw22559 HIV pepti	962	21	42.9	9	6	ABJ48677	151P3D4 C
890	21	42.9	9	4	AAW22563	AAw22563 HIV pepti	963	21	42.9	9	6	ABJ41795	151P3D4 C
891	21	42.9	9	4	AAW22515	AAw22515 HIV pepti	964	21	42.9	9	6	ABJ43635	151P3D4 C
892	21	42.9	9	4	AAW22330	AAw22330 HIV pepti	965	21	42.9	9	6	ABJ45878	151P3D4 C
893	21	42.9	9	4	AAW22560	AAw22560 HIV pepti	966	21	42.9	9	6	ABJ46367	151P3D4 C
894	21	42.9	9	4	AAW22513	AAw22513 HIV pepti	967	21	42.9	9	6	ABJ46368	151P3D4 C
895	21	42.9	9	4	AAW22562	AAw22562 HIV pepti	968	21	42.9	9	6	ABJ42182	151P3D4 C
896	21	42.9	9	4	AAW23240	AAw23240 HIV pepti	969	21	42.9	9	6	ABJ48365	151P3D4 C
897	21	42.9	9	4	AAW49390	AAw49390 Simian im	970	21	42.9	9	6	ABJ44534	151P3D4 C
898	21	42.9	9	4	AAU12507	AAu12507 Human HIV	971	21	42.9	9	6	ABR22789	Human can
899	21	42.9	9	4	AAG61975	Aag61975 Human WT1	972	21	42.9	9	6	ABR22374	Human can
900	21	42.9	9	4	AAG61973	Aag61973 Human WT1	973	21	42.9	9	6	ABR21258	Human can

974 21 42.9 9 6 ABR21390 Human can
975 21 42.9 9 6 ABR24188 Human can
976 21 42.9 9 6 ABR22649 Human can
977 21 42.9 9 6 ABR23772 Human can
978 21 42.9 9 6 ABR20975 Human can
979 21 42.9 9 6 ABR24056 Human can
980 21 42.9 9 7 ADB67360 Human WT1
981 21 42.9 9 7 ADB67373 Human WT1
982 21 42.9 9 7 ADB67492 Mouse WT1
983 21 42.9 9 7 ADB67358 Human WT1
984 21 42.9 9 7 ADB67359 Human WT1
985 21 42.9 9 7 ADBW01531 Drosophila
986 21 42.9 9 7 ADBW01531 Drosophila
987 21 42.9 9 7 ADI07230 101P3A11
988 21 42.9 9 7 ADI08220 101P3A11
989 21 42.9 9 7 ADI06415 101P3A11
990 21 42.9 9 7 ADI07833 101P3A11
991 21 42.9 9 7 ADI08115 101P3A11
992 21 42.9 9 7 ADI08715 101P3A11
993 21 42.9 9 7 ADI05857 101P3A11
994 21 42.9 9 7 ADI06461 101P3A11
995 21 42.9 9 7 ADI08691 101P3A11
996 21 42.9 9 7 ADI05891 101P3A11
997 21 42.9 9 7 ADI07571 101P3A11
998 21 42.9 9 7 ADI06976 101P3A11
999 21 42.9 9 7 ADI07989 101P3A11
1000 21 42.9 9 7 ADI08163 101P3A11
ADZ89103 Immunogen

ALIGNMENTS

RESULT 1
AAB11114
ID AAB11114 standard; peptide; 9 AA.
XX
AC AAB11114;
XX
XX
DT 16-FEB-2001 (first entry)
XX
XX Human MUC-1 protein fragment SEQ ID NO 1.
DE
DE Human; MUC-1; tumor; HLA-A2 restricted immune reaction; treatment;
KW human leukocyte antigen; gene therapy; antigen-presenting cell.
KW
XX Homo sapiens.
XX
XX DE19917195-A1.
XX
XX 19-OCT-2000.
XX
PF 16-APR-1999; 99DE-01017195.
XX
PR 16-APR-1999; 99DE-01017195.
XX
XX (UYTU-) UNIV TUEBINGEN EBERHARD-KARLS.
XX
XX Brossart P, Stevanovic S, Brugger W, Kanz L, Rammensee HG;
XX WPI; 2001-032872/05.
XX
XX New peptide derived from the MUC-1 tumor marker, used to induce a
PT cytotoxic T cell response for treatment or prevention of tumors.
XX
XX Claim 1; Page 6; 8pp; German.

XX This invention describes a novel peptide (I) derived from the MUC-1 gene
CC which is able to induce an HLA (human leukocyte antigen)-A2-restricted
CC immune reaction against tumor cells. (I) or the nucleic acid (II)
CC encoding (I), are used to induce an immune response against tumor cells,
CC so are useful for treatment or prevention of tumors, in conjunction with
CC other tumor therapies. In particular (II) is used in gene therapy or for
CC in vitro transfection or transformation of cells (particularly antigen-

CC presenting cells, optionally in vivo), for expression of (I). (I) has a
CC high binding capacity for HLA-A2 and can reverse the usual suppression of
CC the immune response associated with tumor cells. By introducing the
CC nucleic acid that encodes (I) into an antigen-presenting cell in vitro,
CC then returning the cells to the patient, a more certain and controlled
CC response is achieved, compared with administration of the peptide plus
CC adjuvant

XX Sequence 9 AA;

Query Match 100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPPVHNV 9

Db 1 STAPPVHNV 9

RESULT 2

ABG79089
ID ABG79089 standard; peptide; 9 AA.

XX

AC ABG79089;

XX 15-NOV-2002 (first entry)

DT

DE Human MUC1 class I HLA widely expressed antigen peptide #2.

XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.

OS Homo sapiens.

XX
PN WO200264057-A2.

XX 22-AUG-2002.

XX 15-FEB-2002; 2002WO-US005212.

XX 15-FEB-2001; 2001US-0268687P.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX Wang R;

XX WPI; 2002-627577/67.

XX Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.

XX Disclosure; Page 18; 61pp; English.

XX The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (I) a vaccine comprising (I), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (I) and CPP
CC associated with an antigen for disease, and introducing the antigen-
CC associated CPP to (I), where antigen enters into the cell. The antigen
CC are, for example, tumour antigen derived epitopes recognised by tumour
CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
CC or II. The composition is useful for enhancing immunity in an animal to a
CC disease, by administering a mature dendritic cell comprising CPP
CC associated with an antigen to disease, to the animal, such that following
CC the administration, animal is protected from disease, where the animal
CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a

CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
 CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
 CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
 CC The animal is further subjected to a cancer treatment including surgery,
 CC radiation, chemotherapy or gene therapy. The administration of (II), with
 CC preferably dendritic cell is prior to, subsequent to or concurrent with,
 CC the cancer treatment. The present sequence is a tumour antigen derived
 CC epitope for inclusion in the composition of the invention

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPPVHNV 9
 |||||
 Db 1 STAPPVHNV 9

RESULT 3

ADA50588
 ID ADA50588 standard; peptide; 9 AA.

XX AC ADA50588;

XX DT 20-NOV-2003 (first entry)

XX DE Mucin 1 (MUC-1) CTL epitope, SEQ ID NO:43.

XX KW Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;
 KW humoral response; cellular response; immune response; immunotherapy;
 KW cancer; cytostatic; vaccine; gene therapy; mucin 1; MUC-1;
 KW cytotoxic T lymphocyte; CTL epitope.

XX OS Unidentified.

XX PN WO2003031569-A2.

XX PD 17-APR-2003.

XX PF 18-SEP-2002; 2002WO-US029640.

XX PR 10-OCT-2001; 2001US-0328371P.

XX PA (CENZ) CENTOCOR INC.

XX PI Snyder L, Scallion B, Knight DM, McCarthy SG, Goletz TJ;
 PI Branigan PJ;

XX DR WPI; 2003-393437/37.

XX PT New nucleic acid vaccine, useful for eliciting an immune response to a
 PT cancer associated tumor protein in a mammal.

XX PS Claim 1a; Page 45; 92pp; English.

XX CC The invention relates to a nucleic acid vaccine comprising one or more
 CC tumour antigen-encoding nucleic acids and one or more cytokine adjuvant-
 CC encoding nucleic acids. The tumour antigen encoded by the vaccine is
 CC mucin 1 (MUC-1), the kallikrein KLK2, or prostate specific antigen (PSA,
 CC also known as KLK3), and the cytokine adjuvant encoded can be interleukin
 CC -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),
 CC or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid
 CC is preferably under the control of a promoter such as the cytomegalovirus
 CC immediate early promoter, the dihydrofolate reductase promoter or the
 CC early or late SV40 promoters. The invention also encompasses the method
 CC of eliciting an immune response to a tumour antigen in a mammal using the
 CC vaccine of the invention. Coexpression of the antigen and adjuvant
 CC induces a humoral or cellular response to the tumour antigen, generating
 CC an immune response useful for treatment or prophylaxis of cancers. The
 CC present sequence represents a mucin 1 (MUC-1) polypeptide sequence which

CC is specifically claimed for use in the vaccine of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPPVHNV 9
 |||||
 Db 1 STAPPVHNV 9

RESULT 4

ADG89655

ID ADG89655 standard; peptide; 9 AA.

XX AC ADG89655;

XX DT 11-MAR-2004 (first entry)

XX DE Class I HLA-restricted widely expressed antigen #20.

XX KW metastatic cancer cell differentiation; mutated fibronectin;
 KW metastatic cancer; class I HLA-restricted; widely antigen.

XX OS Unidentified.

XX PN WO2003100027-A2.

XX PD 04-DEC-2003.

XX PF 28-MAY-2003; 2003WO-US016736.

XX PR 28-MAY-2002; 2002US-0383530P.

XX PA (BAYU) BAYLOR COLLEGE MEDICINE.

XX PI Wang R;

XX DR WPI; 2004-035134/03.

XX PT Identifying a cell that differentiates into a metastatic cancer cell,
 PT useful for preventing metastatic cancer, comprises identifying a mutated
 PT fibronectin in the cell.

XX PS Disclosure; SEQ ID NO 98; 137pp; English.

XX CC The invention comprises a method for identifying a cell that will
 CC differentiate into a metastatic cancer cell, the method involves
 CC identifying a mutated fibronectin in the cell. The method of the
 CC invention is useful for preventing metastatic cancer. The present amino
 CC acid sequence represents a Class I HLA-restricted widely expressed
 CC antigen.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPPVHNV 9
 |||||
 Db 1 STAPPVHNV 9

RESULT 5

ADG20359

ID ADG20359 standard; peptide; 9 AA.

XX AC ADG20359;

XX DT 11-MAR-2004 (first entry)

XX DE Antigenic peptide SEQ ID NO:35.
XX AC double-chimeric beta 2-microglobulin; antigenic peptide;
KW antigen-presenting cell; beta 2-microglobulin;
KW major histocompatibility complex class I epitope; MHC class I epitope;
KW cytostatic; antibacterial; virucide; fungicide; protozoacide; vaccine;
KW cytotoxic T lymphocyte induction; cancer; pathogenic organism;
KW tumour associated antigen; pathogenic antigen.
XX Synthetic.
OS WO2003106616-A2.
XX PN 24-DEC-2003.
XX PD
XX PF 12-JUN-2003; 2003WO-IL000501.
XX PR 12-JUN-2002; 2002US-0388273P.
XX PA (GAVI-) GAVISH-GALLILEE BIO APPL LTD.
XX PI Gross G, Margalit A;
XX PF WPI; 2004-071554/07.
XX DR Novel double-chimeric beta2-microglobulin polynucleotide useful for
XX PT treating cancer, comprising sequence encoding polypeptide capable of
XX PT presentation of antigenic peptides.
XX PT
XX PS Claim 16; SEQ ID NO 35; 86pp; English.
XX CC The present invention describes a double-chimeric beta 2-microglobulin
XX CC polynucleotide (I) comprising a sequence encoding a polypeptide (II) that
XX CC is capable of high level presentation of antigenic peptides on antigen-
XX CC presenting cells, where (II) comprising a beta 2-microglobulin molecule
XX CC that is linked through its carboxyl terminal to a polypeptide stretch
XX CC which allows the anchorage of the beta 2-microglobulin molecule to the
XX CC cell membrane, and through its amino terminal to an antigenic peptide
XX CC comprising major histocompatibility complex (MHC) class I epitope. The
XX CC antigenic peptide is not related to an autoimmune disease. Also
XX CC described: (1) an expression vector (III) comprising (I) and is a
XX CC recombinant viral vector; (2) an antigen-presenting cell (IV) transfected
XX CC with (I); (3) a DNA vaccine (V) comprising a (I) or (III); (4) a cellular
XX CC vaccine (VI) for the prevention or treatment of cancer comprising (IV)
XX CC which express (I) or tumour cells transfected with (I), where the cells
XX CC have been pulsed with an antigenic peptide derived from one tumour
XX CC associated antigen; and (5) a pharmaceutical composition (VII) comprising
XX CC (I), (III) or (IV) as an active ingredient and carrier. (I) has
XX CC cytostatic, antibacterial, virucide, fungicide and protozoacide
XX CC activities, and can be used in vaccines, and for inducing cytotoxic T
XX CC lymphocytes. (I) and (V) can be used for the prevention or treatment of
XX CC cancer or for a disease caused by a pathogenic organism. (VI) is useful
XX CC for prevention or treatment of cancer, or disease caused by a pathogenic
XX CC organism, where (VI) presents one tumour associated antigen, or
XX CC pathogenic antigen. (VI) is also useful for immunising a mammal against a
XX CC tumour-associated antigen or a disease caused by a pathogenic organism,
XX CC which involves immunising the mammal with (VI). (I) is useful for
XX CC inducing class I-restricted CTL response in a mammal. The present
XX CC sequence is used in the exemplification of the present invention.

Sequence 9 AA;

Query Match 100.0%; Score 49; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPPVHV 9
Db 1 STAPPVHV 9

RESULT 6

ADU49630
XX ID ADU49630 standard; peptide; 9 AA.
XX AC ADU49630;
XX DT 27-JAN-2005 (first entry)
XX DE Human MUC1 CTL helper epitope sequence.
XX KW PSA; tumour-associated protein; prostate specific antigen; kallikrein-2;
KW KLK2; mucin-1; MUC1; interleukin;
KW granulocyte-macrophage colony-stimulating factor; immunostimulant;
KW cytostatic; vaccine; CTL epitope.
XX OS Homo sapiens.
XX PN WO2004096238-A1.
XX PD 11-NOV-2004.
XX PF 01-APR-2003; 2003WO-US010096.
XX PR 01-APR-2003; 2003WO-US010096.
XX PA (CENZ) CENTOCOR INC.
XX PA (GOLE/) GOLETT T J.
XX PA (MCCA/) MCCARTHY S G.
XX PA (SCAL/) SCALLON B J.
XX PA (SNYD/) SNYDER L A.
XX PA (BRAN/) BRANIGAN P J.
XX PI Goletz TJ, McCarthy SG, Scallon BJ, Snyder LA, Branigan PJ;
XX PI Knight DM;
XX DR WPI; 2004-804620/79.
XX DR N-PSDB; ADU49623.
XX PT Composition comprising polynucleotide encoding antigenic determinant of
XX PT tumor-associated protein (eg prostate specific antigen) and nucleic
XX PT adjuvant (eg interleukin-18) useful for eliciting immune response to
XX PT cancer associated tumor protein.
XX PS Disclosure; SEQ ID NO 52; 105pp; English.
XX CC The invention relates to a new composition that comprises a first
XX CC isolated polynucleotide encoding or complementary to an antigenic
XX CC determinant of a tumour-associated protein and a second isolated
XX CC polynucleotide encoding or complementary to a nucleic acid adjuvant. The
XX CC composition further comprises at least one promoter sequence controlling
XX CC expression of the polynucleotides and a carrier or adjuvant. The promoter
XX CC polynucleotide is human cytomegalovirus immediate early promoter.
XX CC dihydrofolatereductase promoter, early SV40 promoter or late SV40
XX CC promoter. The tumour-associated protein is prostate specific antigen
XX CC (PSA), kallikrein-2 (KLK2) or mucin-1 (MUC1). The nucleic acid adjuvant
XX CC encodes human interleukin (IL)-18 IL-12, granulocyte-macrophage colony-
XX CC stimulating factor or B7-1 or its variant. The first and second
XX CC polynucleotides are contained in the same or separate nucleic acid
XX CC vectors. The composition is useful in eliciting an immune response to a
XX CC cancer associated tumour protein in a mammal. The present sequence
XX CC represents a human MUC1 polypeptide CTL helper epitope.

Sequence 9 AA;

Query Match 100.0%; Score 49; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STAPPVHV 9
Db 1 STAPPVHV 9

RESULT 7

ADX08605
 ID ADX08605 standard; peptide; 9 AA.
 XX AC
 XX ADX08605;
 XX DT
 XX 21-APR-2005 (first entry)
 XX DE
 XX Class I HLA-restricted widely expressed antigen #20.
 XX KW
 XX vaccine; infection; viral infections; virucide; bacterial infection;
 KW antibacterial; yeast infection; fungicide; fungal infection;
 KW protozoal infection; protozoacide; cancer; cytostatic; melanoma;
 KW lung tumor; colon tumor; breast tumor; leukemia; autoimmune disease;
 KW multiple sclerosis; neuroprotective; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; systemic lupus erythematosus; antiinflammatory;
 KW dermatological; immunosuppressive.
 XX OS
 XX Unidentified.
 XX PN
 XX WO2005011730-A1.
 XX PD
 XX 10-FEB-2005.
 XX PF
 XX 30-JUL-2004; 2004WO-GB003285.
 XX PR
 XX 01-AUG-2003; 2003GB-00018096.
 XX PA (UNLO) QUEEN MARY & WESTFIELD COLLEGE.
 XX PI Wang P, Li S;
 XX WPI; 2005-152360/16.
 XX PT New vaccine composition comprises inverted microsomes from animal cells
 PT with an externally disposed peptide antigen and a protein of the Major
 PT Histocompatibility Complex (MHC), useful for treating or preventing, e.g.
 PT cancer.
 XX PS
 XX Disclosure; Page 53; 83pp; English.
 XX CC
 CC The invention comprises a vaccine composition that consists of isolated
 CC inverted microsomes from an animal cell (or its membrane fragments), in
 CC association with an externally disposed peptide antigen and a protein of
 CC the MHC. The vaccine composition of the invention is useful for the
 CC prophylaxis or treatment of: infection (e.g. viral, bacterial, yeast,
 CC fungal or protozoal), cancer (e.g. melanoma, lung adenocarcinoma, colon
 CC cancer, breast cancer or leukemia), autoimmune disease (e.g. multiple
 CC sclerosis, rheumatoid arthritis or systemic lupus erythematosus). The
 CC present amino acid sequence represents a class I HLA-restricted widely
 CC expressed antigen.
 XX SQ
 XX Sequence 9 AA;
 Query Match 100.0%; Score 49; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 STAPPVHNV 9
 Db 1 STAPPVHNV 9
 RESULT 8
 ADY51475
 ID ADY51475 standard; peptide; 9 AA.
 XX AC
 XX ADY51475;
 XX DT
 XX 19-MAY-2005 (first entry)
 XX DE
 XX HLA-A2 peptide modified MUC-1.1 for stimulating cytotoxic T-lymphocytes.
 XX immune stimulation; cytostatic; antimicrobial; antibacterial; virucide;
 KW

KW antiparasitic; cytotoxic T-lymphocyte; major histocompatibility complex;
 KW antigen; cancer; bacterial infection; viral infection;
 KW parasitic infection; CD80.
 XX OS
 XX Homo sapiens.
 XX PN
 XX US2005048646-A1.
 XX PD
 XX 03-MAR-2005.
 XX PF
 XX 29-JUL-2004; 2004US-00901067.
 XX PR
 XX 25-AUG-2003; 2003JP-00341822.
 XX PR
 XX 28-JAN-2004; 2004JP-00020436.
 XX PA (MEDI-) MEDINET CO LTD.
 XX PI
 XX Niede M, Noguchi K, Tadaki T, Sasawatari S;
 XX WPI; 2005-195290/20.
 XX PT
 XX Inducing a cytotoxic T lymphocyte, useful for treating cancer or
 PT infectious disease, comprises contacting a cell line with an antigenic
 PT peptide and a lymphocyte.
 XX PS
 XX Disclosure; Page 7; 29pp; English.
 XX CC
 CC The invention relates to a method of inducing a CTL (cytotoxic T
 CC lymphocyte) by contacting a cell line expressing at least one major
 CC histocompatibility antigen (MHC) class I molecule, an antigen, and a co-
 CC stimulatory molecule, where the cell line is transformed with at least
 CC one co-stimulatory molecule or exogenous antigen, with an isolated or
 CC purified antigenic peptide and with a lymphocyte for a time and under
 CC conditions for inducing a CTL specific for the antigenic peptide. The
 CC method is useful for inducing a CTL. The CTL and method are useful for
 CC treating or preventing cancer or an infectious disease, e.g. a bacterial,
 CC viral, or parasitic infections. The present method provides CTLs having a
 CC high specificity for a disease site, thus allowing a highly effective
 CC treatment. Also, compared to conventional method, the present method uses
 CC a synthetic peptide and thus imposes less burden on the patient. The CTLs
 CC induced using the present method are more likely to function specifically
 CC to individual disease antigens than the CTLs induced conventionally, thus
 CC can be used to stimulate the cytotoxic T-lymphocytes in the method of the
 CC invention. This sequence corresponds to a cancer antigenic peptide to
 CC stimulate the cytotoxic T-lymphocytes by the method of the invention.
 XX SQ
 XX Sequence 9 AA;
 Query Match 100.0%; Score 49; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 STAPPVHNV 9
 Db 1 STAPPVHNV 9
 RESULT 9
 AAR68013
 ID AAR68013 standard; peptide; 9 AA.
 XX AC
 XX AAR68013;
 XX DT
 XX 25-MAR-2003 (revised)
 XX DT
 XX 05-SEP-1995 (first entry)
 XX DE
 XX Mucin peptide p9-17.
 XX KW
 XX Mucin; multiple tandem repeat; vaccine; pancreas cancer; breast cancer;
 KW ovary cancer; colon cancer; HIV.
 XX OS
 XX Synthetic.

PN W09503825-A1.
 XX
 PD 09-FEB-1995.
 XX
 PF 29-JUL-1994; 94WO-US008477.
 XX
 PR 30-JUL-1993; 93US-00099354.
 XX
 PA (FINN/) FINN O J.
 FA (FONT/) FONTENOT J D.
 PA (MONT/) MONTELARO R C.
 XX
 PI Finn OJ, Fontenot JD, Montelaro RC;
 XX
 DR WPI; 1995-082033/11.
 XX
 XX Synthetic multiple tandem repeat mucin-1 peptides and analogues - have
 PT native conformation in the absence of glycosylation and are linked to
 PT epitopes; for vaccines and tests of cancer, viruses and bacteria.
 XX
 PS Disclosure; Page 54; 125pp; English.
 XX
 CC A synthetic peptide such as p105 (AAR68022) includes 5 tandem repeats of
 CC the mucin peptide given in AAR68004. The DTR motif, located between the
 CC first 2 prolines of each repeat, is the target of an anti-mucin immune
 CC response, and can be substituted by a sequence from a virus, tumor
 CC antigen or autoantigen. Drugs based on 9-amino acid portions (AAR68007-
 CC 21) of the mucin peptide were developed. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 9 AA;
 Query Match 79.6%; Score 39; DB 2; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 STAPPVHNV 9
 Db |||||
 1 STAPPANGV 9
 RESULT 10
 ID AAW78844 standard; peptide; 9 AA.
 XX
 AC AAW78844;
 XX
 DT 17-NOV-1998 (first entry)
 XX
 DE MUC-1 protein fragment 9-17.
 XX
 KW Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
 KW class II associated peptide; pathogen; gene therapy; genetic disease;
 KW infection; downregulation; immune response.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN W09831398-A1.
 XX
 PD 23-JUL-1998.
 XX
 PF 22-JAN-1998; 98WO-US001499.
 XX
 PR 22-JAN-1997; 97US-00787547.
 PR 06-JAN-1998; 98US-00003253.
 XX
 PA (PANG-) PANGAEA PHARM INC.
 XX
 PI Hedley ML, Curley JM, Langer RS, Lunsford LB;
 XX
 DR WPI; 1998-427556/36.
 XX

PT New preparations of microparticles - comprising a synthetic polymer
 PT matrix and nucleic acid comprising an expression vector for use in gene
 XX therapy.
 PS Disclosure; Page 10; 101pp; English.
 XX
 CC A microparticle preparation (MP) has been developed, consisting of
 CC microparticles having a diameter of less than 100 mu m. The MP comprises:
 CC (a) a polymeric matrix (PM) consisting of one or more synthetic polymers
 CC having a solubility in water of less than 1 mg/l; and (b) an expression
 CC vector selected from RNA molecules (at least 50% of which are closed
 CC circles) or circular plasmid DNA (at least 50% of which are supercoiled).
 CC Also described is a MP of at most 20 microns in diameter, comprising: (a)
 CC a PM; and (b) a NAM comprising an expression control sequence operatively
 CC linked to a coding sequence, where the coding sequence encodes an
 CC expression product selected from: (i) a polypeptide at least 7 amino
 CC acids in length, having a sequence identical to the sequence of: (i) a
 CC fragment of a naturally-occurring mammalian protein; or (ii) a fragment
 CC of a naturally-occurring protein from an infectious agent which infects a
 CC mammal; (2) a peptide having a length and sequence which permits it to
 CC bind to an MHC class I or II molecule; and (3) the polypeptide or the
 CC peptide linked to a trafficking sequence. AAW69763 to AAW69765, and
 CC AAW78793 to AAW78897 are peptide fragments for use in the present
 CC invention. The MPs are highly effective vehicles for the delivery of
 CC polynucleotides into phagocytic cells. They can be used for gene therapy,
 CC e.g. for treating genetic diseases, infections or tumours or for
 CC downregulating an immune response
 XX
 SQ Sequence 9 AA;
 Query Match 79.6%; Score 39; DB 2; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 STAPPVHNV 9
 Db |||||
 1 STAPPANGV 9
 RESULT 11
 ID AAW72715 standard; peptide; 9 AA.
 XX
 AC AAW72715;
 XX
 DT 11-JAN-1999 (first entry)
 XX
 DE Mucin peptide preparation p 9-17.
 XX
 KW Mucin; muc-1; human; cancer; infectious disease; vaccine; diagnosis;
 KW multiple tandem repeat; pancreatic cancer; breast cancer; colon cancer.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US5827666-A.
 XX
 PD 27-OCT-1998.
 XX
 PF 10-AUG-1994; 94US-00288059.
 XX
 PR 30-JUL-1993; 93US-00099354.
 XX
 PA (UYPI-) UNIV PITTSBURGH.
 XX
 PI Montelaro RC, Fontenot JD, Finn OJ;
 XX
 DR WPI; 1998-593988/50.
 XX
 XX Assay for cancer antibodies - using synthetic peptide comprising multiple
 PT tandem repeats of muc-1.
 XX
 PS Disclosure; Col 25; 45pp; English.

XX An assay has been developed for antibodies to pancreatic, breast or colon
 CC cancer in a sample. The assay comprises contacting the sample with a
 CC synthetic muc-1 peptide that comprises at least two 20 amino acid tandem
 CC repeats of muc-1 and is capable of attaining native conformation in the
 CC absence of glycosylation, and detecting any peptide-antibody complex
 CC formation. The assay can be used in the diagnosis of e.g. pancreatic,
 CC breast or colon cancer. The present sequence represents a mucin peptide
 CC preparation from the present invention
 XX

SQ Sequence 9 AA;

Query Match 79.6%; Score 39; DB 2; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 STAPPVHNV 9
 |||||
 Db 1 STAPPAGGV 9

RESULT 12

ID AAY46704 standard; peptide; 9 AA.

XX AC AAY46704;

XX DT 01-DEC-1999 (first entry)

XX DE Immunogenic peptide having a human leukocyte antigen binding motif #1315.

XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 XX OS immune response; T cell activation; major histocompatibility complex;
 XX KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 XX KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 XX KW vaccine; immunisation.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN W09945954-A1.

XX PD 16-SEP-1999.

XX PF 13-MAR-1998; 98WO-US005039.

XX PR 13-MAR-1998; 98WO-US005039.

XX PA (EPIM-) EPIMUNE INC.

XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

XX DR WPI; 1999-551214/46.

XX PT New immunogenic peptides with HLA binding motif, useful in treatment and
 CC diagnosis of cancers and viral diseases.

XX PS Claim 1; Page 82; 150pp; English.

XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk

CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above
 XX

SQ Sequence 9 AA;

Query Match 79.6%; Score 39; DB 2; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 STAPPVHNV 9
 |||||
 Db 1 STAPPAGGV 9

RESULT 13

AAW67583
 ID AAW67583 standard; peptide; 9 AA.

XX AC AAW67583;

XX DT 02-MAR-1999 (first entry)

XX DE T-cell activation peptide #1.

XX KW Activated T helper cell; CD4+; cytotoxic T cell; CD8+; liposome; epitope;
 XX KW peripheral blood lymphocyte; antigen-presenting cell; APC; virus; tumour;
 XX KW bacterium; parasite; cytokine; vaccine; cancer; malaria; HIV; hepatitis;
 XX KW tuberculosis.

XX OS Synthetic.

XX PN W09850527-A1.

XX PD 12-NOV-1998.

XX PF 07-MAY-1998; 98WO-US009288.

XX PR 08-MAY-1997; 97US-0045949P.

XX PA (BIOM-) BIOMIRA INC.

XX PI Agrawal B, Krantz MJ, Reddish MA, Longenecker BM;

XX DR WPI; 1999-034715/03.

XX PT Method of activation of T cells - by exposure to antigen-presenting cells
 CC loaded with antigen in liposome, used for, e.g. treating cancer and
 CC microbial infections.

XX PS Disclosure; Page 6; 75pp; English.

XX CC Peptides AAW67583-W67611 are used to produce activated T helper (CD4+) and
 CC cytotoxic (CD8+) T cells. The activated T cells are produced by
 CC treating peripheral blood lymphocytes with liposome-encapsulated peptide
 CC antigen to generate Ag-loaded antigen-presenting cells (APC), contacting
 CC naive or anergic T-cells with these APC, and isolating the resulting
 CC activated T-cells. The cells are specific for a particular antigen,
 CC particularly one derived from a tumour, but also those from viruses,
 CC bacteria and other parasites. It can also be used to identify antigens
 CC and epitopes able to generate an Ag-specific T-cell response (by
 CC assessing proliferation and cytokine release). Also the Ag-loaded APC can
 CC be used as cellular vaccines for treating cancer (claimed) or other
 CC diseases (e.g. malaria, human immune deficiency virus infection,
 CC hepatitis, tuberculosis). The activated T-cells can be used to treat the
 CC same conditions by adoptive T-cell transfer therapy
 XX

SQ Sequence 9 AA;

Query Match 79.6%; Score 39; DB 2; Length 9;

Best Local Similarity 77.8%; Pred. No. 2e+06; Mismatches 0; Indels 2; Gaps 0;
Matches 7; Conservative 0

Qy 1 STAPPVHNV 9
Db 1 STAPPAHGV 9

RESULT 14
AAB33656
ID AAB33656 standard; peptide; 9 AA.
AC AAB33656;
XX
XX 26-JAN-2001 (first entry)
XX
XX MHC class I associated immunogenic peptide SEQ ID 55.
XX
XX Microparticle; nucleic acid delivery; immunogenic peptide; MHC I; MHC II;
KW major histocompatibility complex; vaginal tissue; mucosal tissue.
XX
XX Unidentified.
OS
XX WO200053161-A2.
FN
XX
XX 14-SEP-2000.
PD
XX
XX 10-MAR-2000; 2000WO-US006578.
PF
XX
XX 11-MAR-1999; 99US-00266463.
PR
XX 27-MAY-1999; 99US-00321346.
PR
XX (ZYCO-) ZYCOS INC.
PA
XX
XX Lunsford LB, Putnam D, Hedley ML;
PI
XX
XX WPI; 2000-638130/61.
DR
XX
XX Microparticles useful for administering a nucleic acid into the mucosal
PT tissue preferably vaginal tissue of an animal, comprises a polymeric
PT matrix, a lipid and a nucleic acid molecule.
XX
XX Disclosure; Page 14; 96pp; English.
PS
XX
XX The present invention relates to microparticles which are less than 20
CC microns in diameter, which comprise a polymeric matrix, a lipid and a
CC nucleic acid molecule. The microparticle is specifically not encapsulated
CC in a liposome and does not comprise a cell. The nucleotide sequence
CC encodes an expression product that binds to major histocompatibility
CC complex (MHC) type I or II molecules. Peptides AAB33602-B33647 represent
CC MHC class II associated immunogenic peptides, and AAB33648-B33710
CC represent MHC class I associated immunogenic peptides. The peptides are
CC examples of the expression products of the nucleotide sequences which can
CC be included in the microparticles of the invention. Sequences AAB33711-
CC B33716 represent alternative expression products and nuclear localisation
CC signals also used in the invention. The microparticles are useful for
CC administering a nucleic acid into the mucosal tissue preferably vaginal
CC tissue of an animal
XX
XX Sequence 9 AA;
SQ

Query Match 79.6%; Score 39; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 2e+06; Mismatches 0; Indels 2; Gaps 0;
Matches 7; Conservative 0

Qy 1 STAPPVHNV 9
Db 1 STAPPAHGV 9

RESULT 15
AAE09540
ID AAE09540 standard; peptide; 9 AA.

XX AAE09540;
AC
XX
XX 19-NOV-2001 (first entry)
DT
XX
XX DE Human HLA-A*0201 T cell epitope.
DE
XX
XX KW Mucin; cytostatic; immunostimulant; cell mediated immune response;
KW carcinoma; adenocarcinoma; breast cancer; dendritic cell; vaccine;
KW gene therapy; human; HLA-A*0201 T cell epitope.
XX
XX Homo sapiens.
OS
XX WO200157068-A1.
FN
XX
XX 09-AUG-2001.
PD
XX
XX 01-FEB-2001; 2001WO-AU000090.
PF
XX
XX 01-FEB-2000; 2000AU-00005369.
PR
XX 14-JUN-2000; 2000US-00593870.
PR
XX (AUST-) AUSTIN RES INST.
PA
XX
XX Mckenzie IFC, Pietersz GA, Apostolopoulos V;
PI
XX
XX WPI; 2001-541537/60.
DR
XX
XX Immunostimulant peptide, used as an anti-carcinoma vaccine, comprises a
PT an epitope of the non-VNTR, non-leader region of a mucin.
PT
XX
XX Disclosure; Page 23; 84pp; English.
PS
XX
XX The patent discloses peptide or polypeptides capable of eliciting an
CC immune response, comprising an amino acid sequence corresponding to an
CC epitope of the non-central portion of varying numbers of an amino acid
CC motif (VNTR), non-leader region of a mucin. The peptides of the
CC invention, fusion proteins comprising the peptide and conjugate compounds
CC with carbohydrate polymers are used to induce a cell mediated immune
CC response against mucin in the prevention or treatment of carcinoma,
CC preferably adenocarcinoma, most preferably breast cancer. They are also
CC used to pulse dendritic cell for in vivo transfer and use as a vaccine.
CC They are also used in gene therapy. The present sequence is HLA-A*0201 T
CC cell epitope from human. This sequence is used for the prediction of T-
CC cell epitopes for the VNTR region
XX
XX Sequence 9 AA;
SQ

Query Match 79.6%; Score 39; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 2e+06; Mismatches 0; Indels 2; Gaps 0;
Matches 7; Conservative 0

Qy 1 STAPPVHNV 9
Db 1 STAPPAHGV 9

RESULT 16
AAB95902
ID AAB95902 standard; peptide; 9 AA.
ID
XX
XX AAB95902;
AC
XX
XX 25-JUN-2001 (first entry)
DT
XX
XX MHC class-I associated MUC-1 epitope SEQ ID 9.
DE
XX
XX Epitope; tumour antigen; antiviral; immunostimulatory; cervical cancer;
KW human papillomavirus-associated disease; condyloma; cervical dysplasia;
KW cervical dysplasia; major histocompatibility complex; MHC I.
XX
XX Unidentified.
OS
XX

PN WO200119408-A1.
 XX 22-MAR-2001.
 XX 18-SEP-2000; 2000WO-US025559.
 XX 16-SEP-1999; 99US-00398534.
 PR 16-SEP-1999; 99US-0154665P.
 PR 09-DEC-1999; 99US-00458173.
 PR 09-DEC-1999; 99US-0169846P.
 XX (ZYCO-) ZYCOS INC.
 PA Hedley ML, Urban RC, Chicx RM;
 XX WPI; 2001-265996/27.
 DR Novel nucleic acids encoding polypeptide polypeptides containing multiple
 PT epitopes from one or more proteins, useful for treating tumors and as
 PT vaccines against pathogenic agents.
 XX Disclosure; Page 7; 64pp; English.
 XX This invention relates to polynucleotides encoding a hybrid polypeptide
 CC comprising a signal sequence and three segments that are either
 CC contiguous or separated by a spacer amino acid or spacer peptide. The
 CC invention specifically details polynucleotides encoding a polypeptide
 CC peptide where the peptide segments are tumour antigens or a naturally
 CC occurring protein of a pathogenic agent. The polypeptide peptides exhibit
 CC antiviral and immunostimulatory activity. The polynucleotide and
 CC polypeptide peptides are useful for eliciting an immune response in a
 CC mammal. The polynucleotide and protein are useful as vaccines for
 CC treating tumors and pathogenic infections. The polynucleotide is also
 CC useful for preventing or treating human papillomavirus (HPV)-associated
 CC diseases, particularly exophytic condyloma, flat condyloma, cervical
 CC cancer, respiratory papilloma, conjunctival papilloma, genital-tract HPV
 CC infection, cervical dysplasia, high grade squamous intraepithelial
 CC lesions, and anal HPV infection. The polynucleotide and polypeptide are
 CC useful for generating or enhancing prophylactic or therapeutic immune
 CC response against pathogens, tumours or autoimmune diseases in a
 CC population of individuals having diverse MHC allotypes, as positive
 CC controls in T cell stimulation assays in vitro, and as tools to
 CC understand processing of epitopes within cells. Peptides AAB95894 -
 CC AAB96037 and AAB96044 - AAB96048 represent major histocompatibility
 CC complex I (MHC I) associated tumour and pathogen antigens. The peptides
 CC can be used as part of the polypeptide proteins of the invention. Also
 CC included are examples of the polypeptide proteins represented by AAB96050
 CC - AAB96052, and localisation signal peptides AAB96038 - AAB96043 and
 CC AAB96049 which can be used in the construction of the polypeptide
 CC peptides
 XX SQ Sequence 9 AA;
 Query Match 79.6%; Score 39; DB 4; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 STAPPVNVV 9
 Db 1 STAPPAGV 9
 |||||
 RESULT 17
 AAG93752
 ID AAG93752 standard; peptide; 9 AA.
 XX AAG93752;
 AC AAG93752;
 XX 17-SEP-2001 (first entry)
 DT Human MUC-1 peptide.
 DE Continuous flow production; microparticle; gene therapy;
 XX
 KW antisenese therapy; vaccination; treatment; autoimmune disease;
 KW immune response modulation.
 OS Homo sapiens.
 PN WO200136583-A1.
 XX 25-MAY-2001.
 XX 17-NOV-2000; 2000WO-US031770.
 XX 19-NOV-1999; 99US-00443654.
 XX (ZYCO-) ZYCOS INC.
 PA Hedley ML, Hsu Y, Tyo M;
 XX WPI; 2001-425203/45.
 DR Continuous production of microparticles containing nucleic acid for e.g.
 PT gene therapy, comprises mixing a solution of polymeric material and
 PT nucleic acid with a surfactant solution, removing solvent and drying.
 XX Disclosure; Page 11; 47pp; English.
 XX The present sequence is that of a peptide of the invention. The invention
 CC relates to a method for scalable, continuous flow production of a nucleic
 CC acid containing microparticle that maintains the structural integrity of
 CC the associated nucleic acid and results in a microparticle having purity
 CC suitable for introduction into an animal host. Microparticles prepared
 CC according to the method can be used for delivery of a nucleic acid for
 CC gene therapy, antisenese therapy, vaccination, treatment of autoimmune
 CC disease and either specific or non-specific modulation of an immune
 CC response. The microparticles may also be used to deliver nucleic acid
 CC encoding a protein or peptide useful in any kind of therapy. The method
 CC is economical, aseptic and scalable. The method also enables control over
 CC the size of microparticles. The microparticles produced are free of
 CC impurities such as organic solvents and are readily dispersed in a wide
 CC range of dispersing agents
 XX SQ Sequence 9 AA;
 Query Match 79.6%; Score 39; DB 4; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 STAPPVNVV 9
 Db 1 STAPPAGV 9
 |||||
 RESULT 18
 AAB86120
 ID AAB86120 standard; peptide; 9 AA.
 XX AAB86120;
 AC AAB86120;
 XX 23-JUL-2001 (first entry)
 DT Human anti-MUC1 associated-epitope SEQ ID 1.
 DE MUC1; mucin; anti-MUC1; epitope; human; detection; immunogenic; antibody;
 KW breast cancer screening.
 OS Homo sapiens.-
 XX EP1096257-A2.
 XX 02-MAY-2001.
 PD 24-OCT-2000; 2000EP-00123053.
 PF 29-OCT-1999; 99DE-01052160.
 XX PR

XX (SAUE/) SAUER M.
 PA (WOLF/) WOLFRUM J.
 XX Sauer M, Wolfrum J;
 FI WPI; 2001-293137/31.
 DR
 XX Detecting molecules in solution e.g. tumor markers for breast cancer
 PT screening, involves adding dye-labelled binding partner, applying
 PT electric field and detecting dye at anode or cathode.
 XX
 PS Example 1; Page 8; 16pp; German.
 XX
 CC This invention describes a novel method for detecting a molecule (1) in a
 CC solution which involves coupling another molecule (2) with a dye,
 CC selecting the net charge in the solution of dye-labelled molecule to be
 CC opposite to and less than that in the solution of molecule (1), adding
 CC dye-labelled molecule (2) to molecule (1), applying an electric field and
 CC detecting the dye at the anode or cathode (depending on the charge). The
 CC invention also describes a method for detecting a third molecule (3) in a
 CC solution which can bond to molecule (1) and to a second molecule (2) by
 CC coupling dye to (2) and selecting the net charge as above, forming a
 CC complex which can be detected at the cathode if the net charge in the
 CC solution is negative or at the anode if the net charge is positive. This
 CC sequence represents an immunogenic fragment of human MUC1 containing an
 CC epitope which is used to raise anti-MUC1 antibodies, used in screening
 CC for breast cancer. This sequence is used to illustrate the method
 CC described in the invention. The simple and reliable method for the
 CC detection of certain molecules (e.g. anti-MUC1 antibodies or tumor-
 CC specific MUC1 proteins) has a sensitivity 1000 times greater than that of
 CC ELISA tests
 XX
 SQ Sequence 9 AA;
 Query Match 79.6%; Score 39; DB 4; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 STAPPVHNV 9
 Db 1 STAPPAGV 9
 |||||
 |||||
 RESULT 19
 ABG79088
 ID ABG79088 standard; peptide; 9 AA.
 XX
 AC ABG79088;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human MUCI class I HLA widely expressed antigen peptide #1.
 XX
 KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
 KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
 KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
 KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
 KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
 KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
 KW cytostatic; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200264057-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 15-FEB-2002; 2002WO-US005212.
 XX
 PR 15-FEB-2001; 2001US-0269687P.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.

XX Wang R;
 PI WPI; 2002-627577/67.
 DR
 XX Novel composition for treating a disease in an animal, comprises an
 PT immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody.
 XX
 PS Disclosure; Page 18; 61pp; English.
 XX
 CC The invention relates to a composition (I) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
 CC with an antigen, and a pharmaceutically acceptable carrier and (2)
 CC preparing a composition for a disease, by providing (I) and CPP
 CC associated with an antigen for disease, and introducing the antigen-
 CC associated CPP to (I), where antigen enters into the cell. The antigen-
 CC are, for example, tumour antigen derived epitopes recognised by tumour
 CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
 CC or II. The composition is useful for enhancing immunity in an animal to a
 CC disease, by administering a mature dendritic cell comprising CPP
 CC associated with an antigen to disease, to the animal, such that following
 CC the administration, animal is protected from disease, where the animal
 CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
 CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
 CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
 CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
 CC The animal is further subjected to a cancer treatment including surgery,
 CC radiation, chemotherapy or gene therapy. The administration of (I),
 CC preferably dendritic cell is prior to, subsequent to or concurrent with,
 CC the cancer treatment. The present sequence is a tumour antigen derived
 CC epitope for inclusion in the composition of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 79.6%; Score 39; DB 5; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 STAPPVHNV 9
 Db 1 STAPPAGV 9
 |||||
 |||||
 RESULT 20
 AAU82062
 ID AAU82062 standard; peptide; 9 AA.
 XX
 AC AAU82062;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Antigenic peptide M1b associated with cancer (Muc1).
 XX
 KW T-cell binding ligand; TCB; peptide G'; human MHC class II beta chain;
 KW peptide J; human beta-2-microglobulin; HIV-1; TCBL peptide construct;
 KW immunological disorder; immune response; human immunodeficiency virus;
 KW herpes simplex virus infection; HSV; malaria; tuberculosis; cancer; CBA;
 KW acquired immunodeficiency syndrome; AIDS; allergy; autoimmune disease;
 KW acquired immune myocarditis; cytostatic; antiinflammatory.
 XX
 OS Synthetic.
 XX
 PN WO200189286-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 24-MAY-2001; 2001WO-US016793.
 XX
 PR 24-MAY-2000; 2000US-0206548P.
 XX

PA (CELS-) CEL-SCI CORP.
 XX Zimmerman DS, Sarin PS;
 XX WPI; 2002-083037/11.
 XX New T cell binding ligand peptide for treating immunological disorders
 PT such as herpes simplex virus, tuberculosis, cancers, acquired
 PT immunodeficiency syndrome and allergies.
 XX Disclosure; Page 26; 110pp; English.
 XX The present invention relates to novel T-cell binding ligand (TCBL)
 CC peptides (e.g. peptide G' (modified human MHC class II beta chain peptide
 CC G, peptide J (human beta-2-microglobulin peptide) and HIV-1 peptides) and
 CC TCBL peptide constructs for treating immunological disorders. The peptide
 CC constructs are useful for eliciting a cellular immune response in a human
 CC patient. The method comprises administering the peptide construct to the
 CC patient preferably in combination with an immune response adjuvant. The
 CC peptide constructs in the form of conjugated peptides are useful for
 CC eliciting a cellular immune response in a patient exposed to or at risk
 CC for exposure to the human immunodeficiency virus (HIV). The TCBL peptides
 CC are useful for treating a patient suffering from an immunological
 CC disorder such as herpes simplex virus (HSV) infection, malaria,
 CC tuberculosis, cancers, acquired immunodeficiency syndrome (AIDS),
 CC allergies, autoimmune diseases (e.g. arthritis, Graves disease, multiple
 CC sclerosis (MS), autoimmune myocarditis, diabetes and lupus) by
 CC administering a peptide construct comprising a TCBL peptide bonded to an
 CC antigenic peptide associated with the disorder. Unlike prior art peptide
 CC conjugates, a modified version of peptide G has long range stabilisation
 CC and also enhances the immune response. AAU82019-AAU82114 represent T-cell
 CC specific binding ligand peptides, peptide constructs or peptides used in
 CC their construction
 XX Sequence 9 AA;
 SQ

Query Match 79.6%; Score 39; DB 5; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 STAPPVHNV 9
 |||||
 Db 1 STAPPAGGV 9

RESULT 21
 ADA50590
 ID ADA50590 standard; peptide; 9 AA.
 AC ADA50590;
 XX 20-NOV-2003 (first entry)
 DT Mucin 1 (MUC-1) CTL epitope, SEQ ID NO:45.
 DE Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;
 XX humoral response; cellular response; immune response; immunotherapy;
 KW cancer; cytostatic; vaccine; gene therapy; mucin 1; MUC-1;
 KW cytotoxic T lymphocyte; CTL epitope.
 XX Unidentified.
 OS WO2003031569-A2.
 XX 17-APR-2003.
 PD 18-SEP-2002; 2002WO-US029640.
 PF 10-OCT-2001; 2001US-0328371P.
 XX (CENZ) CENTOCOR INC.
 PA Snyder L, Scallon B, Knight DM, McCarthy SG, Goletz TJ;
 PI Microparticles, useful as vehicles for delivery of polynucleotides to

PI Branigan PJ;
 XX WPI; 2003-393437/37.
 XX New nucleic acid vaccine, useful for eliciting an immune response to a
 PT cancer associated tumor protein in a mammal.
 XX Claim 1a; Page 45; 92pp; English.
 XX The invention relates to a nucleic acid vaccine comprising one or more
 CC tumour antigen-encoding nucleic acids and one or more cytokine adjuvant-
 CC encoding nucleic acids. The tumour antigen encoded by the vaccine is
 CC mucin 1 (MUC-1), the kallikrein KLK2, or prostate specific antigen (PSA,
 CC also known as KLK3), and the cytokine adjuvant encoded can be interleukin
 CC -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),
 CC or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid
 CC is preferably under the control of a promoter such as the cytomegalovirus
 CC immediate early promoter, the dihydrofolate reductase promoter or the
 CC early or late SV40 promoters. The invention also encompasses the method
 CC of eliciting an immune response to a tumour antigen in a mammal using the
 CC vaccine of the invention. Coexpression of the antigen and adjuvant
 CC induces a humoral or cellular response to the tumour antigen, generating
 CC an immune response useful for treatment or prophylaxis of cancers. The
 CC present sequence represents a mucin 1 (MUC-1) polypeptide sequence which
 CC is specifically claimed for use in the vaccine of the invention.
 XX Sequence 9 AA;
 SQ

Query Match 79.6%; Score 39; DB 6; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 STAPPVHNV 9
 |||||
 Db 1 STAPPAGGV 9

RESULT 22
 ABU96608
 ID ABU96608 standard; peptide; 9 AA.
 XX ABU96608;
 AC ABU96608;
 XX 12-AUG-2003 (first entry)
 DT MHC class I associated MUC-1 peptide.
 DE Microparticle; microsphere; polynucleotide delivery; phagocytic cell;
 XX tumour; viral infection; bacterial infection; fungal infection;
 KW protozoan infection; gene therapy; major histocompatibility complex;
 KW MHC class I.
 XX Unidentified.
 OS US2002182258-A1.
 XX 05-DEC-2002.
 PD 18-JUL-2001; 2001US-00909460.
 PF 22-JAN-1997; 97US-0035983P.
 XX 06-JAN-1998; 98US-00003253.
 PR 22-JAN-1998; 98WO-US001499.
 PR 11-MAR-1999; 99US-00266463.
 PR 27-MAY-1999; 99US-00321346.
 XX (ZYCO-) ZYCO INC.
 PA Lunsford LB, Putnam D, Hedley ML;
 XX WPI; 2003-438782/41.
 XX Microparticles, useful as vehicles for delivery of polynucleotides to

PT phagocytic cells, comprises polymeric matrix, lipid, and nucleic acid
 PT molecule.
 XX
 PS
 PS
 XX Disclosure; Page 4; 37pp; English.
 XX
 CC The invention relates to a microparticle (microsphere) less than 20
 CC microns in diameter that comprises: (1) a polymeric matrix; (2) a lipid;
 CC and (3) a nucleic acid molecule. The microparticle is not encapsulated in
 CC a liposome and the microparticle does not comprise a cell. The
 CC microparticles are used as vehicles for the delivery of polynucleotides
 CC into phagocytic cells. The microparticles can be used to express antigens
 CC to treat tumour cells or viral, bacterial, fungal or protozoan
 CC infections. The microparticles can be made without adversely affecting
 CC nucleic acid integrity. The present sequence represents the amino acid
 CC sequence of a major histocompatibility complex, MHC, class I associated
 CC peptide
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 79.6%; Score 39; DB 6; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 STAPPVHNV 9
 DB 1 STAPPAGGV 9
 RESULT 23
 ADG89654
 ID ADG89654 standard; peptide; 9 AA.
 XX
 AC ADG89654;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Class I HLA-restricted widely expressed antigen #19.
 XX
 KW metastatic cancer cell differentiation; mutated fibronectin;
 KW metastatic cancer; class I HLA-restricted; widely antigen.
 XX
 OS Unidentified.
 XX
 PN WO2003100027-A2.
 XX
 PD 04-DEC-2003.
 XX
 PF 28-MAY-2003; 2003WO-US016736.
 XX
 PR 28-MAY-2002; 2002US-0383530P.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Wang R;
 XX
 DR WPI; 2004-035134/03.
 XX
 PT Identifying a cell that differentiates into a metastatic cancer cell,
 PT useful for preventing metastatic cancer, comprises identifying a mutated
 PT fibronectin in the cell.
 XX
 PS Disclosure; SEQ ID NO 97; 137pp; English.
 XX
 CC The invention comprises a method for identifying a cell that will
 CC differentiate into a metastatic cancer cell, the method involves
 CC identifying a mutated fibronectin in the cell. The method of the
 CC invention is useful for preventing metastatic cancer. The present amino
 CC acid sequence represents a Class I HLA-restricted widely expressed
 CC antigen.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 79.6%; Score 39; DB 8; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 STAPPVHNV 9
 DB 1 STAPPAGGV 9
 RESULT 24
 ADS87165
 ID ADS87165 standard; peptide; 9 AA.
 XX
 AC ADS87165;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Genetic vaccine/ubiquitin (Ub)/MUC1-related epitope peptide - SEQ ID 181.
 XX
 KW vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma;
 KW Hodgkins lymphoma; non-Hodgkins; leukaemia; neuroblastoma; myeloma;
 KW lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas;
 KW colon; bladder; breast; oesophagus; kidney; brain; epitope; MUC1.
 XX
 OS Unidentified.
 XX
 PN WO2004035085-A1.
 XX
 PD 29-APR-2004.
 XX
 PF 16-OCT-2003; 2003WO-JP013279.
 XX
 PR 17-OCT-2002; 2002JP-00302816.
 XX
 PA (KYUS-) KYUSHU TLO CO LTD.
 XX
 PI Himeno K, Furue M, Maehara Y;
 XX
 DR WPI; 2004-357144/33.
 XX
 PT Gene vaccine containing cancer antigen genes ligated to ubiquitin genes
 PT or cytokine genes for prevention and treatment of cancer.
 XX
 PS Disclosure; SEQ ID NO 181; 266pp; Japanese.
 XX
 CC The invention relates to a novel genetic vaccine containing the ubiquitin
 CC gene together with a gene encoding an antigenic protein containing a T-
 CC cell target sequence. The vaccine of the invention may be useful for
 CC prevention and treatment of cancers including melanoma, sarcoma, lymphoma
 CC (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer
 CC of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas,
 CC colon, bladder, breast, oesophagus, kidney or brain. The current sequence
 CC is that of a genetic vaccine/ubiquitin (Ub)/MUC1-related epitope peptide
 CC of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 79.6%; Score 39; DB 8; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 STAPPVHNV 9
 DB 1 STAPPAGGV 9
 RESULT 25
 ADU49634
 ID ADU49634 standard; peptide; 9 AA.
 XX
 AC ADU49634;
 XX
 DT 27-JAN-2005 (first entry)
 XX

Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 STAPPVHNV 9
 DB 1 STAPPAGGV 9
 RESULT 24
 ADS87165
 ID ADS87165 standard; peptide; 9 AA.
 XX
 AC ADS87165;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Genetic vaccine/ubiquitin (Ub)/MUC1-related epitope peptide - SEQ ID 181.
 XX
 KW vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma;
 KW Hodgkins lymphoma; non-Hodgkins; leukaemia; neuroblastoma; myeloma;
 KW lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas;
 KW colon; bladder; breast; oesophagus; kidney; brain; epitope; MUC1.
 XX
 OS Unidentified.
 XX
 PN WO2004035085-A1.
 XX
 PD 29-APR-2004.
 XX
 PF 16-OCT-2003; 2003WO-JP013279.
 XX
 PR 17-OCT-2002; 2002JP-00302816.
 XX
 PA (KYUS-) KYUSHU TLO CO LTD.
 XX
 PI Himeno K, Furue M, Maehara Y;
 XX
 DR WPI; 2004-357144/33.
 XX
 PT Gene vaccine containing cancer antigen genes ligated to ubiquitin genes
 PT or cytokine genes for prevention and treatment of cancer.
 XX
 PS Disclosure; SEQ ID NO 181; 266pp; Japanese.
 XX
 CC The invention relates to a novel genetic vaccine containing the ubiquitin
 CC gene together with a gene encoding an antigenic protein containing a T-
 CC cell target sequence. The vaccine of the invention may be useful for
 CC prevention and treatment of cancers including melanoma, sarcoma, lymphoma
 CC (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer
 CC of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas,
 CC colon, bladder, breast, oesophagus, kidney or brain. The current sequence
 CC is that of a genetic vaccine/ubiquitin (Ub)/MUC1-related epitope peptide
 CC of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 79.6%; Score 39; DB 8; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 STAPPVHNV 9
 DB 1 STAPPAGGV 9
 RESULT 25
 ADU49634
 ID ADU49634 standard; peptide; 9 AA.
 XX
 AC ADU49634;
 XX
 DT 27-JAN-2005 (first entry)
 XX

DE Human MUC1 CTL helper epitope sequence.
XX
KW PSA; tumour-associated protein; prostate specific antigen; kallikrein-2;
KW KLK2; mucin-1; MUC1; interleukin;
KW granulocyte-macrophage colony-stimulating factor; immunostimulant;
KW cystostatic; vaccine; CTL epitope.
XX
OS Homo sapiens.
XX WO2004096238-A1.
XX
XX 11-NOV-2004.
XX
XX 01-APR-2003; 2003WO-US010096.
XX
XX 01-APR-2003; 2003WO-US010096.
XX (CENZ) CENTOCOR INC.
PA (GOLEZ) GOLETZ T J.
PA (MCCA/) MCCARTHY S G.
PA (SCAL/) SCALLON B J.
PA (SNYD/) SNYDER L A.
PA (BRAN/) BRANIGAN P J.
XX
XX Goletz TJ, McCarthy SG, Scallion BJ, Snyder LA, Branigan PJ;
PI Knight DM;
XX
XX WPI; 2004-804620/79.
DR N-PSDB; ADU49633.
XX
XX Composition comprising polynucleotide encoding antigenic determinant of
PT tumor-associated protein (eg prostate specific antigen) and nucleic
PT adjuvant (eg interleukin-18) useful for eliciting immune response to
PT cancer associated tumor protein.
XX
XX Disclosure; SEQ ID NO 56; 105pp; English.
XX
XX The invention relates to a new composition that comprises a first
CC isolated polynucleotide encoding or complementary to an antigenic
CC determinant of a tumour-associated protein and a second isolated
CC polynucleotide encoding or complementary to a nucleic acid adjuvant. The
CC composition further comprises at least one promoter sequence controlling
CC expression of the polynucleotides and a carrier or adjuvant. The promoter
CC polynucleotide is human cytomegalovirus immediate early promoter,
CC dihydrofolatereductase promoter, early SV40 promoter or late SV40
CC promoter. The tumour-associated protein is prostate specific antigen
CC (PSA), kallikrein-2 (KLK2) or mucin-1 (MUC1). The nucleic acid adjuvant
CC encodes human interleukin (IL)-18 IL-12, granulocyte-macrophage colony-
CC stimulating factor or B7-1 or its variant. The first and second
CC polynucleotides are contained in the same or separate nucleic acid
CC vectors. The composition is useful in eliciting an immune response to a
CC cancer associated tumour protein in a mammal. The present sequence
CC represents a human MUC1 polypeptide CTL helper epitope.
XX
SQ Sequence 9 AA;
Query Match 79.6%; Score 39; DB 8; Length 9;
Best Local Similarity 77.8%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 STAPPVHNV 9
Db 1 STAPPANGV 9
RESULT 26
ADX08604
ID ADX08604 standard; peptide; 9 AA.
XX
XX AC ADX08604;
XX
XX DT 21-APR-2005 (first entry)
XX

DE Class I HLA-restricted widely expressed antigen #19.
XX vaccine; infection; viral infections; virucide; bacterial infection;
KW antibacterial; yeast infection; fungicide; fungal infection;
KW protozoal infection; protozoacide; cancer; cytostatic; melanoma;
KW lung tumor; colon tumor; breast tumor; leukemia; autoimmune disease;
KW multiple sclerosis; neuroprotective; rheumatoid arthritis; antiarthritic;
KW antirheumatic; systemic lupus erythematosus; antiinflammatory;
KW dermatological; immunosuppressive.
XX
OS Unidentified.
XX WO2005011730-A1.
XX
XX 10-FEB-2005.
XX
XX 30-JUL-2004; 2004WO-GB003285.
XX
XX 01-AUG-2003; 2003GB-00018096.
XX (UNLO) QUEEN MARY & WESTFIELD COLLEGE.
XX
XX Wang P, Li S;
XX
XX WPI; 2005-152360/16.
DR
XX
XX New vaccine composition comprises inverted microsomes from animal cells
PT with an externally disposed peptide antigen and a protein of the Major
PT Histocompatibility Complex (MHC), useful for treating or preventing, e.g.
PT cancer.
XX
XX Disclosure; Page 53; 83pp; English.
XX
XX The invention comprises a vaccine composition that consists of isolated
CC inverted microsomes from an animal cell (or its membrane fragments), in
CC association with an externally disposed peptide antigen and a protein of
CC the MHC. The vaccine composition of the invention is useful for the
CC prophylaxis or treatment of: infection (e.g. viral, bacterial, yeast,
CC fungal or protozoal), cancer (e.g. melanoma, lung adenocarcinoma, colon
CC cancer, breast cancer or leukemia), autoimmune disease (e.g. multiple
CC sclerosis, rheumatoid arthritis or systemic lupus erythematosus). The
CC present amino acid sequence represents a class I HLA-restricted widely
CC expressed antigen.
XX
SQ Sequence 9 AA;
Query Match 79.6%; Score 39; DB 9; Length 9;
Best Local Similarity 77.8%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 STAPPVHNV 9
Db 1 STAPPANGV 9
RESULT 27
ADY26204
ID ADY26204 standard; peptide; 9 AA.
XX
XX AC ADY26204;
XX
XX DT 05-MAY-2005 (first entry)
XX
XX DE MHC Class I associated tumor and pathogen peptide, seq id 55.
XX
KW Immunosuppressive; microparticle; gene therapy; antisense therapy;
KW vaccination; autoimmune disease; MHC Class I.
XX
XX OS Homo sapiens.
XX
XX FN US2005037086-A1.
XX
XX DT 17-FEB-2005.

XX 16-JAN-2004; 2004US-00758970.
 XX PF
 XX 19-NOV-1999; 99US-0166516P.
 PR 17-NOV-2000; 2000US-00715708.
 XX (ZYCO-) ZYCOS INC.
 XX PA
 XX Tyo M, Hsu Y, Hedley ML;
 PI WPI; 2005-180376/19.
 XX DR
 XX Scalable continuous preparation of nucleic acid-containing microparticles
 PT to treat autoimmune disease comprises solvent removal device and mixing
 PT chamber; and continuously supplying first emulsion and second aqueous
 PT solution to the chamber.
 XX PS
 XX Disclosure; SEQ ID NO 55; 36pp; English.
 XX CC
 XX The invention relates to the scalable continuous preparation of nucleic
 CC acid-containing microparticles (I) comprising providing a mixing chamber
 CC and a solvent removal device, continuously supplying a first emulsion and
 CC a second aqueous solution to the chamber, continuously transferring the
 CC second emulsion from the chamber to the solvent removal device, and
 CC removing the organic solvent from the second emulsion in the device to
 CC form an aqueous suspension of (I). (I) is used for delivery of a nucleic
 CC acid for gene therapy, antisense therapy, vaccination, treatment of
 CC autoimmune disease, and either specific or non-specific modulation of an
 CC immune response (e.g. via cytokine regulation). The scalable, continuous
 CC flow production of (I) maintains the structural integrity of the
 CC associated nucleic acid and results in a microparticle having a purity
 CC suitable for introduction into an animal (e.g. human) host. The
 CC preparation of (I) provides an economical, aseptic, scalable procedure
 CC for producing a microparticle in amounts necessary for research,
 CC clinical, and other commercial uses. (I) produced using scalable,
 CC continuous flow process contains stable, active, potent, structurally
 CC intact nucleic acid, e.g. as supercoiled DNA. The method also provides
 CC efficient encapsulation of the nucleic acid in the microparticle and
 CC allows for efficient recovery of the microparticle. The current sequence
 CC represents an MHC Class I associated tumor and pathogen peptide sequence.
 CC This sequence could be an expression product of a microparticle of the
 CC invention.
 XX SQ
 XX Sequence 9 AA;
 Query Match 79.6%; Score 39; DB 9; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 STAPPVHNV 9
 |||||
 Db 1 STAPPAGV 9
 RESULT 28
 ADZ66315
 ID ADZ66315 standard; peptide; 9 AA.
 XX AC
 ADZ66315;
 XX DT
 14-JUL-2005 (first entry)
 XX DE
 MUC1 repeat unit (aa 14-20 + 1-2).
 XX KW
 Cytostatic; Aromatase inhibitor; Estrogen agonist; Estrogen antagonist;
 KW MUC1; polymorphic antigen; immunogen; breast cancer; anti-estrogenic;
 KW steroid agent; estrogenic steroid; immunological agent; immune response.
 OS Homo sapiens.
 OS Synthetic.
 XX PN
 WO2005037261-A1.
 XX

PD 28-APR-2005.
 XX 14-OCT-2004; 2004WO-US033988.
 XX PF
 XX 14-OCT-2003; 2003US-0510516P.
 PR 04-JUN-2004; 2004US-0576624P.
 XX (BIOM-) BIOMIRA INC.
 XX PA
 XX Kehoe-Whistance M, Maclean G;
 PI WPI; 2005-322772/33.
 XX DR
 XX Use of synergistic combination of anti-estrogenic steroids and
 PT immunological agents to treat breast cancer.
 PT
 XX Disclosure; Page 28; 103pp; English.
 XX PS
 XX This sequence represents an antigenic peptide derived from the MUC1
 CC repeat unit. MUC1 is a polymorphic antigen characterized by a variable
 CC number (typically 21-125, esp. 41 or 85) of perfect and imperfect repeats
 CC of peptide unit given in ADZ66304. MUC1 fragments may be used as
 CC immunogens in the method of the invention for treatment of breast cancer.
 CC The method comprises the administration of a combination of an anti-
 CC estrogenic steroid agent (A) (effective to reduce the level/activity of
 CC at least one estrogenic steroid) and an immunological agent (B)
 CC (effective to contribute to the development of a protective immune
 CC response to the breast cancer); where (A) and (B) are therapeutically
 CC effective against at least some breast cancers. (B) comprises at least
 CC one immunogen comprising at least one breast cancer-associated epitope;
 CC where at least one epitope is a MUC1 epitope or a carbohydrate epitope.
 CC The immunogen comprises S7n (an STn-KLH conjugate that is an aggregated
 CC conjugate having a NANA content of about 7 %). The antiestrogen comprises
 CC at least one (steroidal/non-steroidal) antiestrogen; where the steroidal
 CC antiestrogen is fulvestrant and the non-steroidal antiestrogen is
 CC toremifene, tamoxifen, droloxifene or trioxifene. The anti-estrogenic
 CC steroid agent comprises at least one aromatase inhibitor
 CC (aminoglutethimide, anastrozole, vorozole, letrozole, liarozole,
 CC megestrol, exemestane or formestane), preferably goserelin acetate or
 CC megesterol acetate. The method further comprises the administration of: at
 CC least one progestin (progesterone) that protects against breast cancer;
 CC at least one anti-progestin that protects against breast cancer; and at
 CC least one chemotherapeutic agent other than an anti-estrogenic steroid
 CC agent, where the chemotherapeutic agent is an anthracycline (doxorubicin,
 CC daunorubicin, epirubicin or idarubicin) or a taxane (paclitaxel or
 CC docetaxel). The combination of (A) and (B) is useful to treat breast
 CC cancer (metastatic breast cancer) and in the manufacture of one or more
 CC compositions for the treatment of breast cancer. (B) is useful in the
 CC manufacture of a composition for the treatment of breast cancer in a
 CC subject who is receiving or has received treatment with an anti-
 CC estrogenic steroid agent, effective to reduce the level or activity of at
 CC least one estrogenic steroid in the subject. (A) is useful in the
 CC manufacture of a composition for the treatment of breast cancer in a
 CC subject who is receiving or has received treatment with an immunological
 CC agent, effective to contribute to the development of a protective immune
 CC response to the breast cancer. The combination of (A) and (B) is
 CC synergistically effective against breast cancer. The combination of (A)
 CC and (B) is effective in the treatment of cancer. The synergistic effect
 CC of the combination of (A) and (B) to treat breast cancer was tested in
 CC patients. The results showed that the patients treated with the immunogen
 CC and the anti-cancer hormone had better time to disease progression (TDP)
 CC and survival outcome when compared to groups treated with (A) or (B)
 CC alone.
 XX SQ
 XX Sequence 9 AA;
 Query Match 79.6%; Score 39; DB 9; Length 9;
 Best Local Similarity 77.8%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 STAPPVHNV 9
 |||||
 Db 1 STAPPAGV 9

RESULT 29
 AAW67603
 ID AAW67603 standard; peptide; 9 AA.
 XX
 AC AAW67603;
 XX
 DT 02-MAR-1999 (first entry)
 XX
 DE Human MUC-1 derived T-cell activation 9-mer peptide.
 XX
 KW Activated T helper cell; CD4+; cytotoxic T cell; CD8+; liposome; epitope;
 KW peripheral blood lymphocyte; antigen-presenting cell; APC; virus; tumour;
 KW bacterium; parasite; cytokine; vaccine; cancer; malaria; HIV; hepatitis;
 KW tuberculosis; mucin.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9850527-A1.
 XX
 PD 12-NOV-1998.
 XX
 PF 07-MAY-1998; 98WO-US009288.
 XX
 PR 08-MAY-1997; 97US-0045949P.
 XX
 PA (BIOM-) BIOMIRA INC.
 XX
 PI Agrawal B, Krantz MJ, Reddish MA, Longenecker BM;
 XX
 DR WPI; 1999-034715/03.
 XX
 PT Method of activation of T cells - by exposure to antigen-presenting cells
 PT loaded with antigen in liposome, used for, e.g. treating cancer and
 PT microbial infections.
 XX
 PS Example 1; Page 30; 75pp; English.
 XX
 CC Peptides AAW67583-W67611 are used to produce activated T helper (CD4+) and cytotoxic (CD8+) T-cells. The activated T cells are produced by treating peripheral blood lymphocytes with liposome-encapsulated peptide antigen to generate Ag-loaded antigen-presenting cells (APC), contacting naive or anergic T-cells with these APC, and isolating the resulting activated T-cells. The cells are specific for a particular antigen, particularly one derived from a tumour, but also those from viruses, bacteria and other parasites. It can also be used to identify antigens and epitopes able to generate an Ag-specific T-cell response (by assessing proliferation and cytokine release). Also the Ag-loaded APC can be used as cellular vaccines for treating cancer (claimed) or other diseases (e.g. malaria, human immune deficiency virus infection, hepatitis, tuberculosis). The activated T-cells can be used to treat the same conditions by adoptive T-cell transfer therapy
 XX
 SQ Sequence 9 AA;
 Query Match 73.5%; Score 36; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 STAPPVHNV 9
 :|||||
 Db 1 ATAPPAGV 9
 RESULT 30
 AAR68012
 ID AAR68012 standard; peptide; 9 AA.
 XX
 AC AAR68012;
 XX
 DT 25-MAR-2003 (revised)

DT 05-SEP-1995 (first entry)
 XX
 DE Mucin peptide p8-16.
 XX
 KW Mucin; multiple tandem repeat; vaccine; pancreas cancer; breast cancer;
 KW ovary cancer; colon cancer; HIV.
 XX
 OS Synthetic.
 OS
 PN WO9503825-A1.
 XX
 PD 09-FEB-1995.
 XX
 PF 29-JUL-1994; 94WO-US008477.
 XX
 PR 30-JUL-1993; 93US-00099354.
 XX
 PA (FINN/) FINN O J.
 PA (FONT/) FONTENOT J D.
 PA (MONT/) MONTELLARO R C.
 XX
 PI Finn OJ, Fontenot JD, Montelaro RC;
 XX
 DR WPI; 1995-082033/11.
 XX
 CC Synthetic multiple tandem repeat mucin-1 peptides and analogues - have native conformation in the absence of glycosylation and are linked to epitopes; for vaccines and tests of cancer, viruses and bacteria.
 XX
 PS Disclosure; Page 54; 125pp; English.
 XX
 CC A synthetic peptide such as p105 (AAR68022) includes 5 tandem repeats of the mucin peptide given in AAR68004. The DTR motif, located between the first 2 prolines of each repeat, is the target of an anti-mucin immune response, and can be substituted by a sequence from a virus, tumor antigen or autoantigen. Drugs based on 9-amino acid portions (AAR68007-21) of the mucin peptide were developed. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 9 AA;
 Query Match 71.4%; Score 35; DB 2; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 STAPPVH 7
 :|||||
 Db 2 STAPPAH 8
 RESULT 31
 AAR68014
 ID AAR68014 standard; peptide; 9 AA.
 XX
 AC AAR68014;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-SEP-1995 (first entry)
 XX
 DE Mucin peptide p10-18.
 XX
 KW Mucin; multiple tandem repeat; vaccine; pancreas cancer; breast cancer;
 KW ovary cancer; colon cancer; HIV.
 XX
 OS Synthetic.
 OS
 PN WO9503825-A1.
 XX
 PD 09-FEB-1995.
 XX
 PF 29-JUL-1994; 94WO-US008477.
 XX
 PR 30-JUL-1993; 93US-00099354.

```

XX (FINN/) FINN O J.
PA (FONT/) FONTENOT J D.
PA (MONT/) MONTELLARO R C.
XX
XX Finn OJ, Fontenot JD, Montelaro RC;
XX
XX WPI; 1995-082033/11.
XX
XX Synthetic multiple tandem repeat mucin-1 peptides and analogues - have
PT native conformation in the absence of glycosylation and are linked to
PT epitopes; for vaccines and tests of cancer, viruses and bacteria.
XX
XX Disclosure; Page 54; 125pp; English.
XX
XX A synthetic peptide such as p105 (AAR68022) includes 5 tandem repeats of
CC the mucin peptide given in AAR68004. The DTR motif, located between the
CC first 2 prolines of each repeat, is the target of an anti-mucin immune
CC response, and can be substituted by a sequence from a virus, tumor
CC antigen or autoantigen. Drugs based on 9-amino acid portions (AAR68007-
CC 21) of the mucin peptide were developed. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 71.4%; Score 35; DB 2; Length 9;
XX Best Local Similarity 85.7%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 TAPPVHV 9
XX      |||||
XX      1 TAPPAHV 8
XX
XX
XX RESULT 32
XX AAR68011
XX ID AAR68011 standard; peptide; 9 AA.
XX
XX AC AAR68011;
XX
XX 25-MAR-2003 (revised)
XX 05-SEP-1995 (first entry)
XX
XX Mucin peptide p7-15.
XX
XX Mucin; multiple tandem repeat; vaccine; pancreas cancer; breast cancer;
XX ovary cancer; colon cancer; HIV.
XX
XX Synthetic.
XX
XX WO9503825-A1.
XX
XX 09-FEB-1995.
XX
XX 29-JUL-1994; 94WO-US008477.
XX
XX 30-JUL-1993; 93US-00099354.
XX
XX (FINN/) FINN O J.
XX (FONT/) FONTENOT J D.
XX (MONT/) MONTELLARO R C.
XX
XX Finn OJ, Fontenot JD, Montelaro RC;
XX
XX WPI; 1995-082033/11.
XX
XX Synthetic multiple tandem repeat mucin-1 peptides and analogues - have
XX native conformation in the absence of glycosylation and are linked to
XX epitopes; for vaccines and tests of cancer, viruses and bacteria.
XX
XX Disclosure; Page 54; 125pp; English.
XX
XX A synthetic peptide such as p105 (AAR68022) includes 5 tandem repeats of

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CC the mucin peptide given in AAR68004. The DTR motif, located between the
CC first 2 prolines of each repeat, is the target of an anti-mucin immune
CC response, and can be substituted by a sequence from a virus, tumor
CC antigen or autoantigen. Drugs based on 9-amino acid portions (AAR68007-
CC 21) of the mucin peptide were developed. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 71.4%; Score 35; DB 2; Length 9;
XX Best Local Similarity 85.7%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 STAPPVH 7
XX      |||||
XX      3 STAPPAH 9
XX
XX
XX RESULT 33
XX AAW72714
XX ID AAW72714 standard; peptide; 9 AA.
XX
XX AC AAW72714;
XX
XX 11-JAN-1999 (first entry)
XX
XX Mucin peptide preparation p 8-16.
XX
XX Mucin; muc-1; human; cancer; infectious disease; vaccine; diagnosis;
XX multiple tandem repeat; pancreatic cancer; breast cancer; colon cancer.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX US5827666-A.
XX
XX 27-OCT-1998.
XX
XX 10-AUG-1994; 94US-00288059.
XX
XX 30-JUL-1993; 93US-00099354.
XX
XX (UYPI-) UNIV PITTSBURGH.
XX
XX Montelaro RC, Fontenot JD, Finn OJ;
XX
XX WPI; 1998-593988/50.
XX
XX Assay for cancer antibodies - using synthetic peptide comprising multiple
XX tandem repeats of muc-1.
XX
XX Disclosure; Col 25; 45pp; English.
XX
XX An assay has been developed for antibodies to pancreatic, breast or colon
XX cancer in a sample. The assay comprises contacting the sample with a
XX synthetic muc-1 peptide that comprises at least two 20 amino acid tandem
XX repeats of muc-1 and is capable of attaining native conformation in the
XX absence of glycosylation, and detecting any peptide-antibody complex
XX formation. The assay can be used in the diagnosis of e.g. pancreatic,
XX breast or colon cancer. The present sequence represents a mucin peptide
XX preparation from the present invention
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 71.4%; Score 35; DB 2; Length 9;
XX Best Local Similarity 85.7%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 STAPPVH 7
XX      |||||
XX      2 STAPPAH 8
XX
XX

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PD	XX	27-OCT-1998.
XX	PF	10-AUG-1994; 94US-00288059.
XX	XX	30-JUL-1993; 93US-00099354.
XX	PA	(UYPI-) UNIV PITTSBURGH.
XX	PI	Montelaro RC, Fontenot JD, Finn OJ;
XX	XX	WPI; 1998-593988/50.
XX	DR	Assay for cancer antibodies - using synthetic peptide comprising multiple tandem repeats of muc-1.
XX	PT	Disclosure; Col 25; 45pp; English.
XX	PS	An assay has been developed for antibodies to pancreatic, breast or colon cancer in a sample. The assay comprises at least two 20 amino acid tandem synthetic muc-1 peptide that comprises at least two 20 amino acid tandem repeats of muc-1 and is capable of attaining native conformation in the absence of glycosylation, and detecting any peptide-antibody complex formation. The assay can be used in the diagnosis of e.g. pancreatic, breast or colon cancer. The present sequence represents a mucin peptide preparation from the present invention
XX	CC	Sequence 9 AA;
XX	SQ	Query Match 71.4%; Score 35; DB 2; Length 9; Best Local Similarity 75.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0
Qy	2	TAPPVHV 9
Db	1	TAPPAHGV 8
RESULT 36		
AAE09534		
ID	AAE09534	standard; peptide; 9 AA.
XX	AC	AAE09534;
XX	XX	19-NOV-2001 (first entry)
XX	XX	Human mucin-1 (MUC-1) VNTR peptide #3.
XX	KW	Mucin-1; cystostatic; immunostimulant; cell mediated immune response; carcinoma; adenocarcinoma; breast cancer; dendritic cell; vaccine; gene therapy; human; MUC-1.
XX	OS	Homo sapiens.
XX	PN	WO200157068-A1.
XX	XX	09-AUG-2001.
XX	PF	01-FEB-2001; 2001WO-AU000090.
XX	PR	01-FEB-2000; 2000AU-00005369.
XX	PR	14-JUN-2000; 2000US-00593870.
XX	PA	(AUST-) AUSTIN RES INST.
XX	PI	Mckenzie IFC, Pieterz GA, Apostolopoulos V;
XX	XX	WPI; 2001-541537/60.
XX	PT	Immunostimulant peptide, used as an anti-carcinoma vaccine, comprises a multiple tandem repeat; pancreatic cancer; breast cancer; colon cancer.
XX	PS	Disclosure; Page 38; 84pp; English.
XX	XX	

PD	XX	27-OCT-1998.
XX	PF	10-AUG-1994; 94US-00288059.
XX	XX	30-JUL-1993; 93US-00099354.
XX	PA	(UYPI-) UNIV PITTSBURGH.
XX	PI	Montelaro RC, Fontenot JD, Finn OJ;
XX	XX	WPI; 1998-593988/50.
XX	DR	Assay for cancer antibodies - using synthetic peptide comprising multiple tandem repeats of muc-1.
XX	PT	Disclosure; Col 25; 45pp; English.
XX	PS	An assay has been developed for antibodies to pancreatic, breast or colon cancer in a sample. The assay comprises at least two 20 amino acid tandem synthetic muc-1 peptide that comprises at least two 20 amino acid tandem repeats of muc-1 and is capable of attaining native conformation in the absence of glycosylation, and detecting any peptide-antibody complex formation. The assay can be used in the diagnosis of e.g. pancreatic, breast or colon cancer. The present sequence represents a mucin peptide preparation from the present invention
XX	CC	Sequence 9 AA;
XX	SQ	Query Match 71.4%; Score 35; DB 2; Length 9; Best Local Similarity 75.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Qy	1	STAPPVH 7
Db	3	STAPPAH 9
RESULT 35		
AAW72716		
ID	AAW72716	standard; peptide; 9 AA.
XX	AC	AAW72716;
XX	XX	11-JAN-1999 (first entry)
XX	XX	Mucin peptide preparation p 10-18.
XX	KW	Mucin; muc-1; human; cancer; infectious disease; vaccine; diagnosis; multiple tandem repeat; pancreatic cancer; breast cancer; colon cancer.
XX	OS	Homo sapiens.
XX	OS	Synthetic.
XX	PN	US5827666-A.
XX	XX	

CC The patent discloses peptide or polypeptides capable of eliciting an
 CC immune response, comprising an amino acid sequence corresponding to an
 CC epitope of the non-central portion of varying numbers of an amino acid
 CC motif (VNTR), non-leader region of a mucin. The peptides of the
 CC invention, fusion proteins comprising the peptide and conjugate compounds
 CC with carbohydrate polymers are used to induce a cell mediated immune
 CC response against mucin in the prevention or treatment of carcinoma,
 CC preferably adenocarcinoma, most preferably breast cancer. They are also
 CC used to pulse dendritic cell for in vivo transfer and use as a vaccine.
 CC They are also used in gene therapy. The present sequence is a VNTR
 CC peptide of mucin-1 (MUC-1) protein from human
 XX
 SQ Sequence 9 AA;

Query Match 71.4%; Score 35; DB 4; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2e+06; Mismatches 0; Gaps 0;
 Matches 6; Conservative 0; Indels 2;

Qy 2 TAPPVHV 9
 |||||
 Db 1 TAPPAHGV 8

RESULT 37
 ADS87178
 ID ADS87178 standard; peptide; 9 AA.

XX
 AC ADS87178;

XX
 DT 18-NOV-2004 (first entry)

XX Genetic vaccine/ubiquitin (Ub)/MUC1-related epitope peptide - SEQ ID 194.

XX vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma;
 KW Hodgkins lymphoma; non-Hodgkins; leukaemia; neuroblastoma; myeloma;
 KW lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas;
 KW colon; bladder; breast; oesophagus; kidney; brain; epitope; MUC1.

XX Unidentified.

XX WO2004035085-A1.

XX 29-APR-2004.

XX 16-OCT-2003; 2003WO-JP013279.

XX 17-OCT-2002; 2002JP-00302816.

XX (KYUS-) KYUSHU TLO CO LTD.

XX Himeno K, Furue M, Maehara Y;

XX WPI; 2004-357144/33.

XX Gene vaccine containing cancer antigen genes ligated to ubiquitin genes
 PT or cytokine genes for prevention and treatment of cancer.

XX Disclosure; SEQ ID NO 194; 266pp; Japanese.

XX The invention relates to a novel genetic vaccine containing the ubiquitin
 CC gene together with a gene encoding an antigenic protein containing a T-
 CC cell target sequence. The vaccine of the invention may be useful for
 CC prevention and treatment of cancers including melanoma, sarcoma, lymphoma
 CC (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer
 CC of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas,
 CC colon, bladder, breast, oesophagus, kidney or brain. The current sequence
 CC is that of a genetic vaccine/ubiquitin (Ub)/MUC1-related epitope peptide
 CC of the invention.

XX Sequence 9 AA;

Query Match 71.4%; Score 35; DB 8; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 STAPPVH 7
 |||||
 Db 2 STAPPAH 8

RESULT 38

ADS87177
 ID ADS87177 standard; peptide; 9 AA.

XX
 AC ADS87177;

XX 18-NOV-2004 (first entry)

XX Genetic vaccine/ubiquitin (Ub)/MUC1-related epitope peptide - SEQ ID 193.

XX vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma;
 KW Hodgkins lymphoma; non-Hodgkins; leukaemia; neuroblastoma; myeloma;
 KW lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas;
 KW colon; bladder; breast; oesophagus; kidney; brain; epitope; MUC1.

XX Unidentified.

XX WO2004035085-A1.

XX 29-APR-2004.

XX 16-OCT-2003; 2003WO-JP013279.

XX 17-OCT-2002; 2002JP-00302816.

XX (KYUS-) KYUSHU TLO CO LTD.

XX Himeno K, Furue M, Maehara Y;

XX WPI; 2004-357144/33.

XX Gene vaccine containing cancer antigen genes ligated to ubiquitin genes
 PT or cytokine genes for prevention and treatment of cancer.

XX Disclosure; SEQ ID NO 193; 266pp; Japanese.

XX The invention relates to a novel genetic vaccine containing the ubiquitin
 CC gene together with a gene encoding an antigenic protein containing a T-
 CC cell target sequence. The vaccine of the invention may be useful for
 CC prevention and treatment of cancers including melanoma, sarcoma, lymphoma
 CC (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer
 CC of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas,
 CC colon, bladder, breast, oesophagus, kidney or brain. The current sequence
 CC is that of a genetic vaccine/ubiquitin (Ub)/MUC1-related epitope peptide
 CC of the invention.

XX Sequence 9 AA;

Query Match 71.4%; Score 35; DB 8; Length 9;
 Best Local Similarity 85.7%; Pred. No. 2e+06; Mismatches 0; Gaps 0;
 Matches 6; Conservative 0; Indels 1;

Qy 1 STAPPVH 7
 |||||
 Db 3 STAPPAH 9

RESULT 39

ADS87166

ID ADS87166 standard; peptide; 9 AA.

XX
 AC ADS87166;

XX 18-NOV-2004 (first entry)

XX Genetic vaccine/ubiquitin (Ub)/MUC1-related epitope peptide - SEQ ID 182.

XX vaccine; ubiquitin; Ub; T-cell target; melanoma; sarcoma;
 KW Hodgkins lymphoma; non-Hodgkins; leukaemia; neuroblastoma; myeloma;
 KW lung cancer; stomach; skin; thyroid; ovary; prostate; womb; pancreas;
 KW colon; bladder; breast; oesophagus; kidney; brain; epitope; MUC1.
 XX Unidentified.
 OS WO2004035085-A1.
 XX PN 29-APR-2004.
 XX PD 16-OCT-2003; 2003WO-JP013279.
 XX PF 17-OCT-2002; 2002JP-00302816.
 XX PR (KYUS-) KYUSHU TLO CO LTD.
 XX PA Himeno K, Furue M, Maehara Y;
 XX PI WPI; 2004-357144/33.
 XX DR Gene vaccine containing cancer antigen genes ligated to ubiquitin genes
 XX PT or cytokine genes for prevention and treatment of cancer.
 XX PT Disclosure; SEQ ID NO 182; 266pp; Japanese.
 XX PS The invention relates to a novel genetic vaccine containing the ubiquitin
 CC gene together with a gene encoding an antigenic protein containing a T-
 CC cell target sequence. The vaccine of the invention may be useful for
 CC prevention and treatment of cancers including melanoma, sarcoma, lymphoma
 CC (Hodgkins or non-Hodgkins), leukaemia, neuroblastoma, myeloma and cancer
 CC of the lung, stomach, skin, thyroid, ovary, prostate, womb, pancreas,
 CC colon, bladder, breast, oesophagus, kidney or brain. The current sequence
 CC is that of a genetic vaccine/ubiquitin (Ub)/MUC1-related epitope peptide
 CC of the invention.
 XX SQ

Query Match 71.4%; Score 35; DB 8; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TAPPVHV 9
 Db 1 TAPPAHV 8

RESULT 40
 ABG73822
 ID ABG73822 standard; peptide; 8 AA.
 XX AC ABG73822;
 XX DT 20-MAR-2003 (first entry)
 XX DE MUC1 associated epitope.
 XX KW Human; MUC1; mucin-1; cytostatic; antagonist; vaccine; tumour;
 KW tumour-associated mucin-1; cancer; breast carcinoma; colon carcinoma;
 KW oesophageal squamous cell carcinoma; pancreatic carcinoma;
 KW prostate carcinoma; multiple myeloma; adenocarcinoma.
 XX OS Homo sapiens.
 XX PN US2002132771-A1.
 XX PD 19-SEP-2002.
 XX PF 26-NOV-2001; 2001US-00994466.
 XX PR 18-AUG-1999; 99US-0149492P.
 PR 11-NOV-1999; 99US-0164714P.

PR 18-AUG-2000; 2000US-00641833.
 PR 28-NOV-2000; 2000US-00724094.
 PR 21-FEB-2001; 2001US-0270456P.
 PR 21-FEB-2001; 2001US-0270471P.
 XX (MADI/) MADIYALAKAN R.
 XX PA Madiyalakan R;
 XX PI WPI; 2003-155898/15.
 XX DR New therapeutic compositions comprising a binding agent that binds to
 XX PT tumor-associated MUC1 epitope, useful for treating human tumors, e.g.
 XX PT breast carcinoma, prostate carcinoma or multiple myeloma.
 XX PS Example 24; Page 13; 27pp; English.
 XX CC The invention relates to new therapeutic compositions, which comprise a
 CC binding agent that specifically binds to an epitope of a tumour-
 CC associated mucin-1 (MUC1), are effective for treating a mammal bearing a
 CC tumour. Mice were implanted with 413BCR tumour cells 2 weeks after the
 CC start of the immunisation series (using either a conjugate of the binding
 CC agent, or a complex of the binding agent-MUC1). It was found that a
 CC humoral response was induced in mice treated with both the conjugated and
 CC complexed binding agent. A T2 cellular response to the binding agent was
 CC induced in these mice. A trend for reduction in tumour mass and size in
 CC mice treated with the conjugated or complexed binding agent was also
 CC demonstrated. The therapeutic compositions or the method is useful for
 CC treating a mammal (particularly a human) bearing a tumour, especially a
 CC tumour that expresses a tumour-associated MUC-1. In particular, the
 CC compositions are useful for treating adenocarcinomas, e.g. breast
 CC carcinoma, colon carcinoma, oesophageal squamous cell carcinoma,
 CC pancreatic carcinoma, prostate carcinoma, or multiple myeloma. The
 CC present sequence represents the mucin-1 associated epitope
 XX Sequence 8 AA;
 SQ

Query Match 65.3%; Score 32; DB 6; Length 8;
 Best Local Similarity 71.4%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STAPPVH 7
 Db 2 TTAPPAH 8

RESULT 41
 AAE26804
 ID AAE26804 standard; peptide; 8 AA.
 XX AC AAE26804;
 XX DT 13-DEC-2002 (first entry)
 XX DE Human HLA-A2.1 restricted MUC-1 (mucin) peptide epitope.
 XX KW Human; cancer; breast cancer; ovarian cancer; melanoma; cell therapy;
 KW epitope; human leucocyte antigen; HLA-A2.1.
 XX OS Homo sapiens.
 XX PN WO200265992-A2.
 XX PD 29-AUG-2002.
 XX PF 19-FEB-2002; 2002WO-US005748.
 XX PR 20-FEB-2001; 2001US-0270252P.
 XX PA (ORTH) ORTHO-MCNEIL PHARM INC.
 XX PI Degraw J, Moriarty A, Leturcq DJ, Jackson MR, Peterson PA;
 PI Heiskala M;

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XX WPI; 2002-667033/71.
XX
XX Treating a subject with cancer comprises combining the CD+8 cells, which
XX are stimulated with non-naturally occurring antigen-presenting cell line,
XX PT with adherent blood monocytes and inoculating the subject with CD8+
XX PT suspension.
XX
XX Example 2; Page 93; 99pp; English.
XX
XX The invention relates to a method of treating a subject with cancer. The
XX method involves combining the CD+8 cells, which are stimulated with non
XX naturally occurring antigen-presenting cell (nnAPC) line, with adherent
XX CC blood monocytes and inoculating the subject with CD8+ suspension. The
XX CC method is useful for treating cancer e.g. ovarian cancer, breast cancer
XX CC and melanoma etc. It is also useful in cell therapy. The present sequence
XX CC is human leukocyte antigen A2 (HLA-A2).1 restricted peptide epitope used
XX CC to treat breast and ovarian cancer
XX
XX Sequence 8 AA;
SQ
    Query Match      64.3%; Score 31.5; DB 5; Length 8;
    Best Local Similarity 88.9%; Pred. No. 2e+06;
    Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 STAPPVHNV 9
        ||| |||||
Db      1 STA-PVHNV 8

RESULT 42
AEA36310
ID AEA36310 standard; peptide; 8 AA.
XX
XX AEA36310;
XX
XX 11-AUG-2005 (first entry)
XX
XX Human MUC-1 950-958 cytotoxic T-lymphocyte epitope peptide.
XX
XX viral infection; virucide; cytostatic; tumor; neoplasm; cell therapy;
XX KW antigen; MUC-1.
XX
XX Homo sapiens.
XX
XX JP2005139118-A.
XX
XX 02-JUN-2005.
XX
XX 07-NOV-2003; 2003JP-00377653.
XX
XX 20-FEB-2001; 2001US-0270252P.
XX
XX (ORTH ) ORTHO-MCNEIL PHARM INC.
XX
XX Leturco DJ, Moriarty AM, Jackson MR, Peterson PA, Richards JM;
XX WPI; 2002-667033/71.
XX
XX Treating a subject with cancer comprises combining the CD+8 cells, which
XX are stimulated with non-naturally occurring antigen-presenting cell line,
XX PT with adherent blood monocytes and inoculating the subject with CD8+
XX PT suspension.
XX
XX Disclosure; SEQ ID NO 20; 65pp; Japanese.
XX
XX The invention relates to a novel method for treating viral infection in a
XX subject. The method comprises preparing an antigen presentation cell
XX CC lineage (nnAPC), collecting CD8+ cells from the subject, stimulating CD8+
XX CC cells using the nnAPC, culturing CD8+ cells in the presence of
XX CC interleukin-2 (IL-2) and/or IL-7, mixing peripheral blood monocytes from
XX CC the subject, subjecting the components to gamma irradiation, combining
XX CC the CD8+ cells with adhesive peripheral blood monocytes and inoculating
XX

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CC the CD8+ suspended solid to the subject. The method of the invention
CC demonstrates virucide and cytostatic activities and may be useful for
CC treating a viral infection or tumor in a subject via cell therapy. The
CC current sequence is that of a human MUC-1 cytotoxic T-lymphocyte epitope
CC peptide of the invention which was incorporated into a Drosophila antigen
CC presenting cell.
XX
XX Sequence 8 AA;
SQ
    Query Match      64.3%; Score 31.5; DB 5; Length 8;
    Best Local Similarity 88.9%; Pred. No. 2e+06;
    Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 STAPPVHNV 9
        ||| |||||
Db      1 STA-PVHNV 8

RESULT 43
AAW38247
ID AAW38247 standard; peptide; 6 AA.
XX
XX AAW38247;
XX
XX 19-MAR-1998 (first entry)
XX
XX Extended region between repeating loops of mucin.
XX
XX Multivalent chimeric peptide; tandem repeat unit; human; mucin 1; MUC1;
XX KW Omega loop sequence; prophylaxis; therapy;
XX KW pathogenic virus neutralisation; human immunodeficiency virus; HIV.
XX
XX Homo sapiens.
XX
XX WO9728187-A2.
XX
XX 07-AUG-1997.
XX
XX 29-JAN-1997; 97WO-US001726.
XX
XX 31-JAN-1996; 96US-00594403.
XX PR 15-OCT-1996; 96US-00730244.
XX
XX (POPU-) POPULATION COUNCIL INC.
XX
XX Fontenot JD, Phillips DM;
XX WPI; 1997-402551/37.
XX
XX New multivalent chimeric peptide(s) for neutralising pathogenic microbes
XX PT - comprising a loop structure of human mucin 1 and an omega loop of an
XX PT immunoglobulin superfamily protein.
XX
XX Disclosure; Page 39; 63pp; English.
XX
XX The present sequence was used in the development of a novel multivalent
XX chimeric peptide, comprising at least 2 tandemly repeated units, where
XX CC the 1st portion of the repeated unit comprises a human mucin 1 (MUC1)
XX CC sequence which forms an extended connector and a base of a loop structure
XX CC of human MUC1, and a 2nd portion comprising an immunoglobulin super
XX CC family protein Omega loop sequence. In the peptide, the natural structure
XX CC of MUC1 tandem repeats can be used to present an Omega loop sequence in a
XX CC functional conformation that is both multivalent and biologically active.
XX CC It can provide prophylactic and therapeutic agents which have the binding
XX CC specificity of an immunoglobulin super family member protein but do not
XX CC have the entire protein's backbone. It can be used to neutralise
XX CC pathogenic viruses, e.g. human immunodeficiency virus (HIV)
XX
XX Sequence 6 AA;
SQ
    Query Match      63.3%; Score 31; DB 2; Length 6;
    Best Local Similarity 83.3%; Pred. No. 2e+06;
    Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2 TAPPVH 7
 DB 1 TAPPAH 6

RESULT 44
 AAB72482
 ID AAB72482 standard; peptide; 6 AA.
 AC AAB72482;
 XX 09-MAY-2001 (first entry)
 DT Fusion protein peptide fragment #16.
 XX Immunomodulatory; human milk fat globule specific antibody; HMPG; cancer;
 KW tumour detection.
 KW Unidentified.
 OS US6190885-B1.
 PN 20-FEB-2001.
 PD 08-OCT-1993; 93US-00134198.
 XX 02-FEB-1990; 90US-00473673.
 PR 08-APR-1993; 93US-00046103.
 XX (CANC-) CANCER RES FUND CONTRA COSTA.
 PA Ceriani RL, Peterson JA, Larocca DJ;
 PI WPI; 2001-217896/22.
 DR Novel fusion protein comprising sequence of amino acids which binds
 XX antibodies specific to human milk fat globule differentiation antigens,
 PT useful as immunogen and for diagnosing breast cancers.
 XX Claim 1; Col 29-30; 37pp; English.
 PS The present invention relates to a fusion protein (see AAB72464) which
 CC substantially fails to bind to human milk fat globule (HMPG) specific
 CC antibody. The fusion protein can be used as an immunogen and for
 CC diagnostic purposes and as part of a kit for detecting the presence of
 CC neoplastic tissue from a solid tumour or metastasis. The present sequence
 CC is a peptide which was used in the present invention

QY 2 TAPPVH 7
 DB 1 TAPPAH 6

Query Match 63.3%; Score 31; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAPPVH 7
 DB 1 TAPPAH 6

RESULT 45
 AAY82854
 ID AAY82854 standard; peptide; 9 AA.
 XX AAY82854;
 XX 19-JUN-2000 (first entry)
 DT Mucin peptide fragment (tumour associated antigen).
 XX Tumour associated antigen peptide; TAA; cancer; carcinoma; treatment;
 KW prevention; cure; anti-tumour vaccine; metastases; breast; bladder;
 KW prostate; pancreas; ovary; thyroid; colon; stomach; carcinoma;

KW MHC Class I; HLA-A2; human; Major Histocompatibility Complex; uroplakin;
 KW prostate specific antigen; prostate specific membrane antigen;
 KW prostate acid phosphatase; mucin; lactadherin;
 KW teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPTO-1.
 XX Homo sapiens.
 OS WC200006723-A1.
 PN 10-FEB-2000.
 PD 29-JUL-1999; 99WO-IL000417.
 XX 30-JUL-1998; 98IL-00125608.
 PR (YEDA) YEDA RES & DEV CO LTD.
 PA (BIOT-) BIO-TECHNOLOGY GEN CORP.
 XX Eisenbach L, Carmon L, Tirosh B, Bar-Haim E, Paz A, Fridkin M;
 PI Fitzer-Attas C;
 PI WPI; 2000-205463/18.
 DR Tumor associated antigen peptides, especially derived from uroplakin,
 XX useful as vaccines to prevent or cure cancers including breast, bladder,
 PT prostate, pancreas, ovary, thyroid, colon and stomach.
 PS Claim 15; Page 102; 113pp; English.
 XX Tumour associated antigen peptides (TAA) may be used for the treatment,
 CC prevention and cure of cancer or cancer metastases. The cancer may be
 CC breast, bladder, prostate, pancreas, ovary, thyroid, colon, stomach, head
 CC or neck cancer or a carcinoma. The tumour associated antigens are
 CC presentable to the immune system by HLA-A2 molecules and are generally
 CC between 8 to 10 amino acids in length. The amino acids located at
 CC positions 2 and 9 of the tumour associated antigens are the anchor
 CC residues which participate in the binding to MHC class I molecules, more
 CC specifically HLA-A2. More tumour associated antigens are described in
 CC GENESQ records AAY82806-Y82882. Those tumour associated antigens
 CC described in records AAY82806-Y82824 and AAY82855-Y82869 are derived
 CC from Uroplakin, such as Uroplakin II, Uroplakin Ia, Uroplakin III and
 CC Uroplakin Ib. Those described in records AAY82825-Y82829 are derived from
 CC prostate specific antigen (PSA). Those described in records AAY82830-
 CC Y82835 are derived from prostate specific membrane antigen (PSMA). Those
 CC described in records Y82836-AAY82839 are derived from prostate acid
 CC phosphatase (PAP). Those described in records AAY82840-Y82846 are derived
 CC from Lactadherin (LA-46). Those described in records AAY82847-Y82854 are
 CC derived from Mucin and those described in records AAY82871-Y82882 are
 CC derived from Teratocarcinoma derived growth factor (CRIPTO-1)

QY 1 STAPPV 6
 DB 4 STAPPV 9

Query Match 63.3%; Score 31; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STAPPV 6
 DB 4 STAPPV 9

RESULT 46
 AAU00540
 ID AAU00540 standard; peptide; 9 AA.
 XX AAU00540;
 AC AAU00540;
 XX 12-SEP-2001 (first entry)
 DT Human MUC1 polypeptide derivative #1.
 XX Human; MUC1; antigenic peptide; major histocompatibility complex; MHC-I;
 KW glycoprotein; cytotoxic T lymphocytes; T cell response; cancer; vaccine;

KW cancer gene therapy; diagnosis; treatment; inflammatory disorder;
KW organ transplant rejection; graft versus host disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 2..9
FT /note= "Epitope"
XX
PN WO200118035-A2.
XX
XX 15-MAR-2001.
PD
XX
XX 07-SEP-2000; 2000WO-EP008761.
PF
XX 08-SEP-1999; 99GB-00021242.
PR 10-SEP-1999; 99EP-00402237.
PR 03-MAR-2000; 2000US-0187215P.
XX
XX (TRGE) TRANSGENE SA.
PA (INCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
PA Taylor-Papadimitriou J, Heukamp LC, Offringa R, Melief CJM;
PI Acres B, Thomas M;
PI
XX WPI; 2001-235187/24.
DR N-PSDB; AAS00586.
DR
XX
XX New antigenic polypeptides of MUC-1 protein which activate cytotoxic T
PT lymphocyte proteins and their analogs, useful for identifying a major
PT histocompatibility complex class I restricted T cell response and for
PT diagnosing cancer.
XX
XX Claim 2; Page 6; 8lpp; English.
PS
XX The sequence represents a human MUC1 polypeptide derivative. Derivative
CC antigenic peptides of MUC1 protein bind at least one major
CC histocompatibility complex class I (MHC-I) glycoprotein, which activates
CC cytotoxic T lymphocytes to induce a protective response against tumours.
CC Diagnosis of cancer involves determining the presence or absence in a
CC host cell of MHC class I restricted T cell response to a MUC1 derivative,
CC where the presence of the MHC class I restricted T cell response
CC indicates that the host has cancer. Measurement of the level of MHC class
CC I restricted T cell response is also useful to monitor the severity of
CC cancer, a larger response indicating a more severe cancer. MUC1
CC derivatives are useful in cancer therapy and to follow MUC1 specific
CC immune responses in patients during the course of disease and/or
CC treatment. MUC1 DNA is useful in cancer gene therapy, vaccination and
CC diagnosis. Compositions of the sequences are used in vaccines and
CC treatments against cancer or diseases caused by an immune response, such
CC as an inflammatory disorder, organ transplant rejection or graft versus
CC host disease
XX
SQ Sequence 9 AA;
Query Match 63.3%; Score 31; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 STAPPV 6
Db 4 STAPPV 9
RESULT 47
ADB84181
ID ADB84181 standard; peptide; 9 AA.
XX
AC ADB84181;
XX
XX 04-DEC-2003 (first entry)
DT
XX Human MUC1-derived peptide MUC(167-175) SEQ ID NO:8.
DE

XX human; immune system; immunostimulatory; CpG dinucleotide;
KW immunostimulant; MUC1.
XX
OS Homo sapiens.
XX
PN WO2003066649-A1.
XX
XX 14-AUG-2003.
PD
XX 04-FEB-2003; 2003WO-CA000135.
PF
XX 04-FEB-2002; 2002US-0353195P.
PR
XX (BIOM-) BIOMIRA INC.
PA
XX Jiang Z, Koganty RR, Yalamati D, Baek M;
PI
XX WPI; 2003-767230/72.
DR
XX Stimulation of immune system involves administration of immunostimulatory
PT molecule comprising at least one oligonucleotide strand having at least
PT one nucleotide sequence and at least one covalently incorporated
PT lipophilic group.
XX
XX Disclosure; Page 85; 95pp; English.
PS
XX The invention relates to a novel method for stimulating an immune system.
CC The method involves administering an immunostimulatory molecule of
CC covalently lipidated oligonucleotides comprising the CpG dinucleotide
CC unit, or an analogue. The method of the invention has immunostimulant
CC activity. The invention is useful in the manufacture of a composition for
CC immunostimulating a subject. The present sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 9 AA;
Query Match 63.3%; Score 31; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 STAPPV 6
Db 4 STAPPV 9
RESULT 48
ADD88876
ID ADD88876 standard; peptide; 9 AA.
XX
AC ADD88876;
XX
XX 29-JAN-2004 (first entry)
DT
XX Human MUC1 peptide SEQ ID NO:8.
DE
XX glycolipopeptide; cytostatic; antibacterial; virucide; antiparasitic;
KW vaccine; gene therapy; immunotherapeutic; cancer; cross-reactive epitope;
KW immune response; parasite; MUC1.
XX
XX Homo sapiens.
XX
XX WO2003089574-A2.
PN
XX 30-OCT-2003.
PD
XX 09-APR-2003; 2003WO-US010750.
PF
XX 15-APR-2002; 2002US-0372105P.
PR 06-MAY-2002; 2002US-0377595P.
XX
XX (BIOM-) BIOMIRA INC.
PA
XX

XX 21-DEC-2000.
PD
XX 15-JUN-2000; 2000WO-CA000711.
PF
XX 15-JUN-1999; 99US-0139263P.
PR
XX (UYHE-) UNIV HEALTH NETWORK.
PA
XX Gariepy J, Yang S;
PI
XX WPI; 2001-091388/10.
DR
XX
XX Novel ligands that binds to MUC1, an epithelial cell mucin, useful for
PT diagnosing, monitoring, treating and preventing cancer.
FT
XX Example 2; Page 26; 60pp; English.
PS
XX
XX The present sequence represents a peptide derived from a human MUC1
CC protein. MUC1 is an epithelial cell mucin, which is found on, and shed
CC from, the surface of many tumours. The specification describes ligands
CC that bind to MUC1. These ligands were isolated using a phage display
CC technique using MUC1 tandem repeats as the target. The MUC1 tandem target
CC repeats comprise repeats of the peptide AAB31258. The ligands are useful
CC for detecting the presence of MUC1 in a sample, to treat or prevent
CC cancer associated with MUC1 and to prepare a medicament or diagnostic
CC agent to treat, prevent or detect cancer associated with MUC1. By
CC assaying for the binding between the MUC1 ligand and MUC1 in a sample
CC diagnosis or monitoring of cancer can be carried out. The ligands may
CC also be used to prepare antibodies
XX
SQ Sequence 8 AA;
Query Match 61.2%; Score 30; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. NO. 2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 APPVHNV 9
Db 1 APPAHGV 7

Search completed: February 24, 2006, 10:14:28
Job time : 208 secs